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October 1, 2004, 20:50:35; Search time 128 Seconds (without alignments) 869.717 Million cell updates/sec
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1 MFCPLKLILLPVLLDYSLGL.....RNNSLEKKSGGGMPKTQQAF 394
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Listing first 45 summaries
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Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping. ¥ AAY66764 standard; protein; 394 Membrane-bound protein PRO1387. 98US-0087607P.
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The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques
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N-PSDB; AA265110.
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Yuan J;
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PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120
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                                                                     KGESQVFKKAVVLHVLPEBPKELMVHVGGLIQMGCVFQSTEVKHVTKVFWIFSGRRAKEE
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23-MAR-1999;
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, costeoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic vasculitis, arcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases of the central and prisease, gluten-sensitive enteropathy and Whipple's disease, autoimmune cor immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AACS8397 to AACS8397 to AACS8397 to AACS8397 to AACS8397 to AACS83414 to AAB33477 represent human PRO polymucleotide and protein sequences given in the ceremony.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
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iive 0; Mismatches 0;
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20-DEC-1999; 99WO-US030095.
30-DEC-1999; 99WO-US0300999.
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06-JAN-2000; 2000WO-US000277.
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11-FEB-2000; 2000WO-US003565.
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12-MAR-1999;
28-APR-1999;
14-MAY-1999;
02-JUN-1999;
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01-SEP-1999;
08-SEP-1999;
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12-JAN-1999
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                                                                180
                                                                                                                             240
                                                                                                                                                            LVPKKTIVLHVSPREPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC 300
                                                                                                                                                                                                                         GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360
                                                                                                                                                                                                                                           GNKSSVNSTVLVKNTKKTNPEIKBKPCHFBRCGGEKHIYSPIIVREVIEEEEPSEKSEAT 360
PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inflammation; rheumatoid arthritis; Crohn's disease; asthma; multiple sclerosis; allergy; AIDS; diabetes mellitus antiinflammatory; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human inflammation-associated polypeptide useful for diagnosis, prevention and treatment of inflammatory diseases comprises product of gene coexpressed with e.g. CD16, L-selectin and IP-30.
                                                 IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN
                                                                                                                                                                               241 LVFKKTIVLHVSBEBEPRILVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC
                             KGESQVFKKAVVJHVLPBEPKELMVHVGGLIQMGCVFQSTBVKHVTKVBWIFSGRRAKE
                                                                                             IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN
                                                                                                                                                                                                                                                                                       YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394
                                                                                                                                                                                                                                                                                                        361 YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human inflammation associated protein #11
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AAU12431 standard; protein; 394 AA.

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Claim 72; Fig 92; 315pp; English.
99WO-US020944.
99WO-US021090.
99WO-US021547.
99WO-US023089.
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Best Local Similarity 100.
Matches 394; Conservative
                                             Ashkenazi AJ, Baker KP,
Goddard A, Godowski PJ,
                                                  A, Goucas, Watanabe CK,
                                 (GETH ) GENENTECH INC.
                                                                   WPI; 2000-412154/35.
                                                                                                                                                                                              present invention
                                                                                                                                                                                                        Sequence 394 AA;
                                                                         N-PSDB; AAA77683
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
29-OCT-1999;
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Smith V,
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Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
                                                                                                     Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                       Human PRO1387 polypeptide sequence
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18-FEB-2000; 2000MO-US004342.
22-FEB-2000; 2000MO-US004414.
24-FEB-2000; 2000MO-US004914.
24-FEB-2000; 2000MO-US0056014.
01-MAR-2000; 2000MO-US005601.
02-MAR-2000; 2000MO-US005601.
03-MAR-2000; 2000MO-US005841.
15-MAR-2000; 2000MO-US006884.
20-MAR-2000; 2000MO-US006884.
21-MAR-2000; 2000MO-US006884.
21-MAR-2000; 2000MO-US006884.
21-MAR-2000; 2000MO-US014042.
30-MAY-2000; 2000MO-US014941.
02-JUN-2000; 2000MO-US014941.
02-JUN-2000; 2000MO-US014941.
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99WO-US030999.
99WO-US031243.
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                                                         (first entry)
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Smith V, Ster
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16-DEC-1999;
20-DEC-1999;
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30-DEC-1999;
30-DEC-1999;
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                                                         24-OCT-2001
                            AAU12431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGEHAKDEYVLYYYSVILSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120
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                                                                                                                                                                                                                                          Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
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100.0%; Pred. No. 5.1e-188;
tive 0; Mismatches 0;
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Klein RD,
Wood WI;
                                                                                                                                    , Ferrara N,
r, Gurney AL,
Williams PM,
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RESULT 5 AAU12431

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AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, prostate, rectal, cervical or liver tumours by comparing PRO of the 275 sequences are also useful to stimulate the release of tumour cf the 275 sequences are also useful to stimulate the release of tumour differentiation of chondrocytes, the proliferation or gene expression in proliferation of inner ear utricular supporting cells or of T. (PBMCs), or the proliferation of endothelial cells or of T. (PBMCs), or the proliferation of endothelial cells or of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal colls or by adipocytes; or inhibit binding of A-peptide to factor involved in binding interactions. The polymucleotides encoding PRO colypeptides can be used in assays to identify molecules collypeptides can be used to generate probes, antisense RNA/DNA, vy
                             Claim 12; Fig 520; 813pp; English.
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100.0%; Score 2067; DB 4; Length 394; 100.0%; Pred. No. 5.1e-188; cive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                     YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF
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1 MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS
                                                                          PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLGDVQEADQGTYICEIRL
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                                                                                                                                                                                                                                          100.0%; Score 2067; DB 4; Length 394; 100.0%; Pred. No. 5.1e-188; tive 0; Mismatches 0; Indels 0
                      Matches 394; Conservative
          Similarity
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Query Match
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                                                                                                                                                                                                  Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
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Gaps

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous cof the invention may be used to treat diseases of the peripheral nervous cof the invention may be used to treat diseases, peripheral nervous cof system, such as peripheral nervous injuries, peripheral nervous cof localised neuropathies and central nervous system disease, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the cutilisation of the activities such as: Immune system suppression, atilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and constant of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                         Wang D;
   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J,
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Yang Y,
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Xue AJ,
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Drmanac RT;
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25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00693036.
                                                                                                                                                                                                                                                                                                                                                                                rang YT, Liu C, Asundi V,
Wang J, Wang Z, Wehrman T,
Zhou P, Goodrich P
                                                                                                                                                              26-DEC-2000; 2000WO-US034263
                                                                                                                                                                                                   99US-00471275
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N-PSDB; AAI58016.
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                                                                 Homo sapiens
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PRO polynucleotides used to produce polypeptides used to target bioactive
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Paoni NF;
Wood WI;
                                                                                                                      LVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILLIVKKTC 300
                       241 LVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
                                                                                            GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eaton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO1387 (UNQ722) protein sequence SEQ ID NO:422.
                                                                                                                                                                                                 YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394
                                                                                                                                                                                                                                    AAB65287 standard; protein; 394 AA
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05-JAN-2000;

06-JAN-2000;

11-FEB-2000;

2000WO-US000376.

11-FEB-2000;

22-FEB-2000;

24-FEB-2000;

24-FEB-2000;

25-FEB-2000;

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27-FEB-2000;

27-FEB-2000;
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99US-0141037P.
99US-0143048P.
99US-0144758P.
99US-0145698P.
99US-0146222P.
99US-0149396P.
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99US-0158663P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic assay
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28-JUL-1999;
17-AUG-1999;
15-SEP-1999;
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08-OCT-1999;
30-NOV-1999;
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16-DEC-1999;
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The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can proteins. The PRO proteins have cytostatic activity. The PRO proteins can cadiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to in the exemplification of the present invention
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molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
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0
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Best Local Similarity 100.0%; Score 2067; DB 4;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394
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                                                   Claim 12; Fig 304; 935pp; English.
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                                                                                                                                                                                                                                                                                                                        Sequence 394 AA;
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PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120

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28-UUL-2000; 2000WS-U220893P.
28-UUL-2000; 2000WS-U220425P.
22-AUG-2000; 2000WS-0222425P.
23-AUG-2000; 2000WS-022133P.
23-AUG-2000; 2000WS-US023328.
10-NOV-2000; 2000WS-US03646P.
10-NOV-2000; 2000WS-US03646P.
10-DEC-2000; 2000WS-US032678.
20-DEC-2000; 2000WS-US032678.
20-DEC-2000; 2000WS-US034956.
28-FEB-2001; 2001WS-US034956.
                                              2000US-0220585P.
2000US-0220605P.
2000US-0220607P.
2000US-0220638P.
2000US-0220638P.
                                                                                           2000US-0220666P.
2000US-0220893P.
2000WO-US020710.
                        29-JUN-2001; 2001WO-US021066
                                                                                                                                                                                                       22-MAR-2001; 2001US-00816744.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001WO-US017092.
                                                                                                                                                                                                                                                           Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                   WPI; 2002-172001/22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 394 AA;
                                                                                    25-JUL-2000; 2
25-JUL-2000; 2
26-JUL-2000; 2
        31-JAN-2002
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The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The Requences of the 122 PRO polypucleotides.

Concode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder.

Concor, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation of differentiation of chondrocyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO protein sequences of the invention
                                                                                                                                                                                                                                                                                          One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor.
        Goddard A, Godowski PJ;
phan JF, Watanabe CK, Wood WI;
Gerritsen ME, Goddard
Smith V, Stephan JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 196; 359pp; English.
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1 MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS

100.0%; Score 2067; DB 5; Length 394; 100.0%; Pred. No. 5.1e-188; ive 0; Mismatches 0; Indels 0.

Matches 394; Conservative

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Similarity

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                      Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; throwbophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
                                                 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE
                                                                                      KGESQVFKKAVVLHVLPEBPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE
                                                                       181 IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN
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                                                                                                                                                                                                                              Human PRO1387 protein sequence SEQ ID NO:234.
                                                                                                                                                                                                                                                                                             ABBB4933 standard; protein; 394
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2000WO-US023328.
2000US-0230978P.
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2001US-00767609.
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2000US-0222695P.
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2000US-00665350.
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2000WO-US030952
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28-JUL-2000;
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28-FEB-2001;
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GODOWSKI P J.
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(GODD/)
(GODO/)
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(FERR/)
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                                                                                                                                                                                                                                                                                                                                       ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGEHAKDEYVLYYYSNLSVPIGRPQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120
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                                                                                                                                                                                           , Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                       One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 2067; DB 5; Length 394; 100.0%; Pred. No. 5.1e-188; ative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the present invention
                                                                                                                                                                                                                                                                                                                      Claim 11; Fig 234; 565pp; English.
                                          2001US-00816744.
2001US-00828366.
2001US-00854208.
2001US-00854280.
2001US-00866028.
2001US-00866034.
           2001WO-US006666.
2001US-00802706.
2001US-00808689.
                                                                                                                         2001US-00870574.
2001WO-US017443.
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Matches 394; Conservative
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28-FEB-2001; 2
01-MAR-2001; 2
09-MAR-2001; 2
14-MAR-2001; 2
22-MAR-2001; 2
05-APR-2001; 2
10-MAY-2001; 2
10-MAY-2001; 2
25-MAY-2001; 2
25-MAY-2001; 2
25-MAY-2001; 2
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Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
antiarteriosclerotic.
301 GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360
                                                                                                                                                                                                                                                                                                                                                                     Human angiogenesis related protein PRO1387 SEQ ID NO: 234.
                                                      YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394
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07-SEP-2000; 2000WS-US0230378P.
18-SEP-2000; 2000US-US0230378P.
18-SEP-2000; 2000US-US664610.
24-OCT-2000; 2000US-US42922P.
08-NOV-2000; 2000WS-US030952.
10-NOV-2000; 2000WS-US030952.
10-NOV-2000; 2000WS-US030873.
01-DEC-2000; 2000WS-US030873.
01-DEC-2000; 2000WS-US030873.
01-DEC-2000; 2000WS-US034956.
22-JAN-2001; 2001US-US06666.
09-MAR-2001; 2001US-US066689.
22-MAR-2001; 2001US-US086689.
22-MAR-2001; 2001US-US0866028.
25-MAY-2001; 2001US-US0866028.
25-MAY-2001; 2001US-US866028.
25-MAY-2001; 2001US-US866028.
25-MAY-2001; 2001US-US866034.
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2001WO-US017800
2001WO-US019692
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02-AUG-2000; 2000US-0222695P.
17-AUG-2000; 2000US-00643657.
23-AUG-2000; 2000WO-US023522.
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FERRARA N.
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30-MAY-2001; 2
01-JUN-2001; 2
20-JUN-2001; 2
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Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
antibody-dependent enzyme mediated prodrug therapy.
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970S-006511P-
970S-0065311P-
970S-0065311P-
970S-0065311P-
980S-0078910P-
980S-0087559P-
980S-0087759P-
980S-0088021P-
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980S-008916P-
980S-0089538P-
                                                                                                                                                                                      15-NOV-2001; 2001US-00997666
                                   Human PRO polypeptide #134
         14-APR-2003 (first entry)
                                                                                                                                    US2003027163-A1.
                                                                                                              Homo sapiens.
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28-MAY-1998;
02-JUN-1998;
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17-JUN-1
18-JUN-1
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                                                                                                                             Gerber H, Gerritsen ME, Goddard A;
L, Hillan KJ, Marsters SA, Pan J, Paoni NF;
CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardialinfarction), endothelial or angiogenic disorders in a mammal.
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100.0%; Score 2067; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                  Claim 11; Fig 234; 567pp; English.
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                                                                                                                                          Godowski PJ, Gurney AL,
Stephan JF, Watanabe CK,
GURNEY A L.
HILLAN K J.
MARSTERS S A.
PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
                                                                                                                             Ferrara N,
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N-PSDB; ABL95677.
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Godowski P
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(MARS/)
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                                                             (STEP/)
(WATA/)
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(WOOD/)
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	DB .1e-1 s	LTVHVGDS; LTVHVGDS;	SDILCN SDILCN	MGCVF	RNDG
	2067 No. natch	PPE 	FONRVHLMGDILC FONRVHLMGDILC	VGGLI(FONRVNLVGDIF
	Score Pred.	SECTINDENVS	<u>R—R</u>	EPKELMVHVGGLIQMGC 	HFONRY HFONRY
98US-0098014P. 98US-0100634P. 98US-0100634P. 98US-0100858P. 98US-0100858P. 98WO-US019437. 98WO-US021141. 98WO-US021141. 99WO-US021141. 99WO-US021141. 99US-0113296P. 99US-0141037P. 99US-0141037P. 99US-0145698P. 99US-0146222P. 99US-0146222P. 99US-01462313. 99US-0146232P. 99US-014623P. 99US-014639P. 99US-014639P. 99US-014639P. 99US-0146313. 99WO-US028313. 99WO-US028313. 99WO-US004341.	0.0%; 0.0%; e 0	OYSLGL OYSLGL	rulyyysnlsvpi	FKKAVVLHVLPEEP FKKAVVLHVLPEEP	YSQSWGHFC YSQSWGHFC
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LVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLLPVLILIVKKTC 300

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Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
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N-PSDB; ABX80392.
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06-JAN-2000;
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28-JUL-2000;
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17-MAY-2000;
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30-MAY-2000;
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16-JUN-1998;
16-JUN-1998;
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16-SEP-1998;
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01-DEC-1998;
05-JAN-1999;
08-MAR-1999;
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Roy MA, C
     GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360
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                                                                                                                                                                           Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.
                          Novel human secreted or transmembrane protein PRO1387.
                                                    394
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Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
98US-0088826P.
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Godowski PJ; Paoni NF; Wood WI;

ABU82692 standard; protein; 394 AA.

on of stimulated T-lymphocytes immune response and in cancer

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The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in polypeptides are useful in detecting PRO polypeptides in a sample, in in modulating at least one biological activity of a cell expressing a PRO in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO136 and PRO136 cuseful for treating candiac prophlary endothelial growth, and PRO536, PRO43, PRO43, PRO43, PRO436, PRO43, PRO437 induce c-fos in endothelial growth, and are thus useful for treating cancerous tumours. PRO512 inhibits vascular cuseful for treating cancerous tumours. PRO512 inhibits vascular cuseful for treating cancerous tumours. PRO512 inhibits vascular cuseful for inhibiting endothelial growth factor (VEGE) stimulated proliferation of mammals which would be beneficial in inhibiting tumour growth. PRO826, Cells and is thus useful for inhibiting endothelial growth. PRO528, PRO528 PRO1375, which stimulate proliferation therapeutically useful for enhancing in Claim 12; Fig 304; 648pp; English treatments.

Sequence 394 AA;

0 240 300 240 300 GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360 PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120 180 180 09 9 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN LVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC LVPKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN 1 MFCPLKLILLPVLLDYSLGINDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS 0; Gaps 100.0%; Score 2067; DB 6; Length 394; 100.0%; Pred. No. 5.1e-188; Indels ô YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394 YMIMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394 0; Mismatches Query Match Best Local Similarity 100. Matches 394; Conservative 181 301 301 361 361 121 121 181 241 241 61 g òγ à g 8 Op ð g 8 a $\dot{\delta}$ В ठ

RESULT 13 ABU82692

Human; PRO; secreted protein; transmembrane protein; cardiac insufficiency disorders; angiogenesis; wound healing; cancerous tumour; immune response; retinal disorder; sight loss; retinitis pigmentosum; age-related macular degeneration; AMD; kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis; Crohn's disease; sports injury; arthritis. Human secreted/transmembrane protein PRO1387 98US-0088021P. 98US-0088021P. 98US-0088026P. 98US-0088026P. 98US-0088039P. 98US-0088030P. 98US-0088030P. 98US-0088167P. 98US-0088212P. 98US-0088212P. 98US-0088216P. 98US-0088216P. 98US-0088216P. 98US-0088216P. 98US-008821P. 98US-008821P. 98US-008821P. 98US-008821P. 98US-008821P. 98US-008821P. 98US-008821P. 98US-008851P. 98US-008881P. 98US-008881P. 98US-008881P. 98US-0089538P. 98US-0089598P. 98US-0089599P. 98US-0089801P. 98US-0089907P. 98US-0089908P. 98US-0075945P 98US-0078910P 98US-0083322P 98US-0084600P 98US-00B7607P 98US-0087609P 98US-0087759P 2001US-00990711 97WO-US020069 (first entry) US2003032023-A1 02-JUN-1998; 02-JUN-1998; 03-JUN-1998; 04-JUN-1998; 04-JUN-1998; 04-JUN-1998; 04-JUN-1998; 04-JUN-1998; 04-JUN-1998; 04-JUN-1998; 05-JUN-1998; 05-JUN-1998; Homo sapiens. 14-NOV-2001; 18-JUN-1998 1998; 05-JUN-1998 10-JUN-1998 1998 10-JUN-1998 1998 11-JUN-1998 11-JUN-1998 17-JUN-1998 18-JUN-1998 24-NOV-1997; 25-FEB-1998; 28-APR-1998 07-MAY-1998 28-MAY-1998 -JUN-1998 16-JUN-1998 17-JUN-1998 12-NOV-1997 13-NOV-1997 13-FEB-2003 26-JUN-2003 ABU82692, -NUL-01 10-JUN-10-JUN-10-JUN-

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181 IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN 240
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ABU60611 standard; protein; 394 AA.

ABU60611;

Filvaroff E, Gao W; Deforge L, Desnoyers L, Filvaroff E, G, A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Beresini M, IE, Goddard Stewart TA, 2003-341980/32. N-PSDB; ACD24112 Baker KP, Bere Gerritsen ME, Smith V,

New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, axquired immunodeficiency syndrome (AIDS), or cancer.

Claim 12; Fig 520; 660pp; English.

The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one CC of 275 nucleotide sequences, and which encodes a corresponding polypeptide selected from 275 amino acid sequences. Where all sequences of 1275 nucleotides, link a bioactive molecule to a cell sequences are given in the specification. The polypeptide corocade by (I) is used to Getect PRO polypeptides, link a bioactive molecule to a cell expressing a release of tumour necrosis factor (TMP)-alpha from human blood, modulate the uptake of glucose or free fatty acid by cells, stimulate or inhibit the proliferation or differentiation of cells or gene expression, the proliferation or differentiation of cells or gene expression, atimulate the release of proteoglycans, stimulate the release of cytokine from peripheral blood monouclear cells, inhibit the binding of A-peptide coid and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atheroscierosis, cardiac injury, infertility, brith defects, premature aging, acquired immunodeficiency syndrome coid sources, or diabetic complications. The nucleic acid is useful as attisense RNA or DNA. The polypeptides are useful as pharmaceuticals, chis is the amino acid sequence of a novel human secreted and complicatione. XX

Sequence 394 AA;

ò PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120 240 PGEHAKDEYVLYYYSNLSVPIGRFONRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE 180 GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEFPSEKSEAT 360 1 MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS 60 9 1 MFCPLKLILLPVLLDYSLGINDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS LVEKKTIVLHVSPEBPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN Gaps .; 0 100.0%; Score 2067; DB 6; Length 394; 100.0%; Pred. No. 5.1e-188; ive 0; Mismatches 0; Indels 0. YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394 Best Local Similarity 100. Matches 394; Conservative 19 121 181 61 121 181 241 Query Match 241 301 301 361 8 g 8 g ₹ ద 8 δ õ g

RESULT 15

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secreted; transmembrane; signal peptide; pharmaceutical;
                                                   Human secreted/transmembrane protein, #170
                                                                        diagnostic; therapeutic; gene therapy
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97US-0065311P

98US-0065311P

98US-0083322P

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98US-0088025P

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98WO-US021141
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is also available in electronic format from USPTO at sequenta.uspto.gov/sequence.html

Sequence 394 AA;

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99WO-US000106.
99WO-US005028.
99WO-US012552.
99WO-US021090.
99WO-US028313.
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98WO-US025108
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05-JAN-1999;
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16-DEC-1999;
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02-MAR-2000;
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DL; Godowski PJ; Paoni NF; Wood WI; Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang Z;

WPI; 2003-288106/28. N-PSDB; ABX90370.

New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.

Claim 12; Fig 304; 650pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polymentication, as chromosome markers, or in generating probes. The PRO identification, as chromosome markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for protucts. The sequences presented in ABU60478-ABU60624 are the PRO polymucleotides of the invention. Note: The sequence data for this patent

ô GNKSSVNSTVLVKNTKKTNPEIKERPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360 120 120 180 180 240 240 09 09 241 LVFKKTIVLHVSPEBPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLFVLLIJVKKTC IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN LVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC 1 MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS PGEHAKDEYVLYYSULSVPIGREQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL KGESQVFKKAVVIHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE 1 MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS Gaps 0; Length 394; 0; Indels 100.0%; Score 2067; DB 6; 100.0%; Pred. No. 5.1e-188; iive 0; Mismatches 0; YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394 Matches 394; Conservative Query Match Best Local Similarity 61 121 301 301 361 361 181 241 g 엄 ò g δ ద à à g ò ð g

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Aaz65110 Membrane-
Aas77683 Human PRO
Aaf4256 Human CDN
Abk33633 CDNA enco
Ab188188 Human PRO
Ab195677 Human ang
Abx80393 Novel hum
Aca69299 Human CDN
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The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith V, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Membrane-bound proteins and related nucleotide sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 303; 822pp; English.
          98US - 0095916P

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Yuan J;
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Wood WI,
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Matches 1630; Conservative 0; Mismatches 0; Indels 0;

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The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenesis and cardiovascularisation, andiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent inventional invention of the protein sequences used in the exemplification of the
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                                                                                                                                                                                                                                        Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
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A, Godowski PJ, Gurney AL,
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                                                                                                                                                                                        Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                      Human cDNA sequence encoding for PRO1387 polypeptide.
                                                                                                                  AAS21503 standard; cDNA; 1630 BP
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AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides are useful to detect other PRO polypeptides to link bioactive molecules to cells expressing PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, coloppeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in periotyte cells, the release of proteoglycans from cartilage, the periotyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide encoding PRO (VIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymucleotides encoding PRO polypeptides can be used in gene therapy
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                                                                                                                                                                                             Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
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                   (GETH ) GENENTECH INC
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                                                                                                              proteins. The PRO proteins have cytostatic activity. The PRO proteins can radiolabels or targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
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cancer; colon cancer;

breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha; gene; ss. secreted protein; PRO; tumour; lung 2000WO-US020710. 2000US-0222425P. 2000US-0227133P. 2000US-0253646P. 2000WO-US032678. 2000US-00747259. 2000WO-US034956. 29-JUN-2001; 2001WO-US021066 WPI; 2002-172001/22. P-PSDB; AAU83689. 20-DEC-2000; 28-FEB-2001; 201-MAR-2001; 22-MAR-2001; 210-MAY-2001; 25-MAY-2001; 25-MAY-2001; 2 23-AUG-2000; 24-AUG-2000; 10-NOV-2000; 28-NOV-2000; 25-JUL-2000; 25-JUL-2000; 25-JUL-2000; 25-JUL-2000; 25-JUL-2000; 26-JUL-2000; 28-JUL-2000; 28-JUL-2000; Homo sapiens 22-AUG-2000; 31-JAN-2002 useful as lung or live Baker One

2000WO-US023522. 2000WO-US023328. 2000WO-US030873.

2001WO-US006520. 2001WO-US006666.

2001US-00816744

2001US-00854208, 2001US-00854280,

2001WO-US017092

2000US-0220664P. 2000US-0220666P.

2000US-0220893P

2000US-0220624P

2000US-0220607P

(GETH) GENENTECH INC

A, Godowski PJ; Watanabe CK, Wood WI; Gerritsen ME, Goddard A, Smith V, Stephan JF, Wa Ľ, AĽ, Desnoyers Gurney Grimaldi JC,

b hundred and twenty two nucleic acids encoding PRO polypeptides, stul for treating a PRO related disorder and for diagnosing tumors such lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor liver tumor.

Claim 2; Fig 195; 359pp; English.

The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of of for stimulating the release of tumour necrosis factor-alpha from human blood, the proliferation of inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABR3336-ABR33657 represent human PRO sequences of the invention coding protein

BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other; Sequence 1630

1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCTGCCATTTTGAAAAGATGT 1080 ATATTGATCGTGAAGAGCCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGGTG 1020 540 AArcagiriegigarcarreregaarrerereregeeaareereceeereceeereere ô 540 099 720 720 780 780 840 840 900 960 240 360 480 480 900 600 360 420 420 120 120 180 180 240 TTCAAGATAGACTGGGACTCTGTCACCAGGAGGACGCCAAGGACGAATATGTGTGCTATAC 300 300 09 ATATTGATCGTGAAGACCTGTGGAATAAGAGTTCAGTGAATTCTACAGTCTTGGTG TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC TTCAAGATAGACTGGGACTCTGTCACCAGGAGGAGGACGAAGGACGAATATGTGCTATAC 301 TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGG ATGGGATGTTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATT GTGGAGTACTCCCAGAGCTGGGGCCCACTTCCAGAATCGTGTGAACCTGGTGGGGGGACATT Greekeracreccaeaecreeeceaerrecaeareerereaaecereereereeree trececaateaceetrecateatectreaegaeteaegaeteaeateaeaaaetae TCAGGACGGCGCAAAGGAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT Accrecagnarccaccnagggaaccregrerrcaagaaaaccarrerecrecage AATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTCCTGTTCTG CATGIGGGIGATICAGCICTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATA TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGG GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA ACCTATATCTGTGAAATCCGCCTCAAAGGGGAAGAGCCAGGTGTTCAAGAAGGCGGTGGTA ATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATT readdacedecedeaaagdagaararrearrearracraccacaaacreaggargrer TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTAC ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAAGAAAACCATTGTGCTGCATGTCAGC CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGGTCTTGGGTGGT TIGGAITIGAAAGTIGAGAGCAGCAIGITITGCCCCACTGAAACTCATCCTGCTGCCAGTG TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCCGCCTGAGCTAACAGTC CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAGACAAATGTATA 361 gacarcriargcaargargcrerererecrecaagargrecaagagegega CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC Gaps .; 0 Length 1630; Indels 9 .; 0 DB ö Mismatches 100.0%; Score 1630; 100.0%; Pred. No. 0; . 0 Query Match Best Local Similarity 100. Matches 1630; Conservative 721 901 901 196 781 841 841 196 541 601 661 721 781 241 241 301 421 421 481 481 541 601 661 121 121 181 181 361 61 Н -61 à g ઠ g δ Q ò g δ g 2 8 δ g 8 ద ò g 엄 ò d ð δ g ò g q ⋩ d à Db ò 셤 8 8

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ABL88188 standard; cDNA; 1630 ABL88188; ABL88188
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BP

(first entry) 16-MAY-2002

Human PRO1387 cDNA sequence SEQ ID NO:233.

Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.

Homo sapiens

WO200200690-A2

03-JAN-2002

20-JUN-2001; 2001WO-US019692

23-JUN-2000; 2000US-0213637P. 20-JUL-2000; 2000US-0219556P.

20-DEC-2000; 2000WO-US034956. 22-JAN-2001; 2001US-00767609. 28-FEB-2001; 2001US-00796498. 28-FEB-2001; 2001WO-US006520. 01-MAR-2001; 2001WO-US006666. 09-MAR-2001; 2001US-00808689. 22-MAR-2001; 2001US-00816744. 05-APR-2001; 2001US-00816744. 2000US-022695P. 2000US-00643657. 2000WO-US023522. 2000US-0230978P. 2000US-00664610. 2000US-00664610. 2000US-0066328. 2000US-0066330. 2000WO-US030952. 2000WO-US030952. 2000WO-US030873. 25-MAY-2001; 2001US-00866034. 25-MAY-2001; 2001WO-US017092. 30-MAY-2001; 2001US-00870574. 30-MAY-2001; 2001WO-US017443. 10-MAY-2001; 2001US-00854208. 10-MAY-2001; 2001US-00854280. 25-MAY-2001; 2001US-00866028. 01-JUN-2001; 2001WO-US017800 (GETH) GENENTECH INC. 18-SEP-2000; 18-SEP-2000; 24-OCT-2000; 08-NOV-2000; 08-NOV-2000; 10-NOV-2000;

Paoni NF; SA, Pan J, Goddard A; Baker KP, Ferrara N, Gerber H, Gerritsen ME, G Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Stephan JF, Watanabe CK, Williams PM, Wood WI,

WPI; 2002-090516/12.

P-PSDB; ABB84933.

One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.

Claim 2; Fig 233; 565pp; English.

ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention

Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

.; 0 DB 6; Length 1630; 0; Indels 100.0%; Score 1630; 100.0%; Pred. No. 0; ive 0; Mismatches Best Local Similarity 100. Matches 1630; Conservative Query Match

9 9 1 cederice Adrica de contraca 1 CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC

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25-JUL-2000; 2000US-0220624P.
28-JUL-2000; 2000US-0220664P.
28-JUL-2000; 2000WO-US020710.
02-AUG-2000; 2000US-022695P.
17-AUG-2000; 2000US-022695P.
23-AUG-2000; 2000WO-US02352.
24-AUG-2000; 2000WS-0230978P.
18-SEP-2000; 2000US-00664610.
18-SEP-2000; 2000US-00665350.
24-OCT-2000; 2000US-02665350.
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                 TCAGATCGGAACAACTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA
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Page 11

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The present sequence is a coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                    Gerber H, Gerritsen ME, Goddard A;
L, Hillan KJ, Marsters SA, Pan J,
CK, Williams PM, Wood WI, Ye W;
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08-NOV-2000; 2000WO-US030952.
10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000WO-US034956.
22-JAN-2001; 2001US-00767609.
28-FEB-2001; 2001US-00767609.
28-FEB-2001; 2001US-0076666.
09-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-0081674.
05-APR-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854208.
25-MAY-2001; 2001US-00856028.
25-MAY-2001; 2001US-00856028.
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01-JUN-2001; 2001WO-US017800.
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GERRITSEN M E.
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.

Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

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TIGGAITIGAAAGTIGAGAGCAGCAIGITITIGCCCACTGAAACTCATCCTGCTGCCAGIG 120

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                                                                                        CTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGACTGGAC
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                    TCAGATCGGAACAACTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA
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hypertrophy of neonatal heart; angiogenesis; wound healing;
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(GETH) GENENTECH INC.

DL; Godowski PJ; Paoni NF; Wood WI; Baker KP, Botstein D, Desnoyers L, Eaton ong S, Gerber H, Gerritsen ME, Goddard A, Gurney AL, Kljavin IJ, Napier MA, Pan J, art TA, Tumas D, Watanabe CK, Williams PM, Ferrara N, Fong S, Grimaldi JC, Gurney Roy MA, Stewart TA, Ashkenazi AJ, .; Z Zhang

WPI; 2003-247083/24

P-PSDB; ABU59181

isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 PRO1375, which stimulate proliferation of stimulated T-lymphocytes therapeutically useful for enhancing immune response and in cancer treatments Novel and are

Claim 2; Fig 305; 648pp; English

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO336, PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126, PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth. PRO826, mammals which would be beneficial in inhibiting tumour growth.

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            stimulated T-1ymphocytes and are therapeutically useful for enhancing immune response. PROB28, PROB26, PRO1132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation or of photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD. PROB19, PROB13 and PRO11066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PROB14, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and arthus useful for treating sports injuries, and arthritis. This sequence represents a novel human PRO protein polynucleotide
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cardiac insufficiency disorders; angiogenesis; wound healing;
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cancerous tumour; immune response; retinal disorder; sight loss; retinitis pigmentosum; age-related macular degeneration; AMD; kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis; Crohn's disease; sports injury; arthritis.
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is factor (TNF)-alpha release;
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re; atherosclerosis;
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(GETH) GENENTECH INC

The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one CC has 80 % sequences, and which encodes a corresponding of 275 nucleotide sequences, and which encodes a corresponding collise given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing a coll et ct umour necrosis factor (TNF) alpha from human blood, modulate the release of tumour necrosis factor (TNF) alpha from human blood, modulate the proliferation or differentiation of cells, stimulate or inhibit to stimulate the release of proteoglycans, stimulate the release of proteoglycans, stimulate the release of proteoglycans, cardiac from peripheral blood monounclear cells, inhibit the binding of A-peptide to factor VIIA, or detect the presence of tumour in a mammal. The nucleic coll seases, organ failure, atherosclerosis, cardiac injury, infertility, diseases, organ failure, atherosclerosis, are useful as pharmaceuticals, disagnostics, biosensors or bioreactors. Both are useful and New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, axquired immunodeficiency Gao W; Deforge L, Desnoyers L, Filvaroff E, G, A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Claim 2; Fig 519; 660pp; English. syndrome (AIDS), or cancer. Beresini M, Æ, Goddard ME, Goddard Stewart TA, WPI; 2003-341980/32. P-PSDB; ABO17875. polypeptide Gerritsen Smith V,

DB 7; Length 1630; Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other; Query Match Best Local Similarity

0 120 180 240 240 300 300 360 360 420 9 CATGTGGGTGATTCAGCTCTGATGGGATGTTTTCCAGAGCACAGAAGACAAATGTATA TTCAAGATAGACTGGGACTCTGTCACCAGGAGGACGCCAAGGACGAATATGTGCTATAC TIGGATITIGAAAGTIGAGAGCAGCAIGITITIGCCCCACTGAAACTCATCCTGCTGCCAGTG TAACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC TTCAAGATAGACTGGGCTCTGTCACCAGGAGGACGCCAAGGACGAATATGTGCTATAC CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC ceecrceaerecaererreseaaarrreaerecarrecercecereserecrerreare Trigaritigaaadrigaagcagcargritigcccacrgaaacrcarccrgcracra TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC CATGTGGGTGATTCAGCTCTGATGGGATGTTTTCCAGAGCACAGAAGACAAATGTATA TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGG TATTACTCCAATCTCAGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGG GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGAGTGTGCAAGAGGCTGACCAGGGA ., Indels .; 0 100.0%; Score 1630; 100.0%; Pred. No. 0; ative 0; Mismatches Matches 1630; Conservative 61 121 121 181 181 241 241 301 361 19 301 qq à 셤 Š a ò g δ Ωp g ò ò

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421 ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCCAGGTGTTCAAGAAGGCGGTGGTA 480

361 GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA

Db 1501 ACACTGGCCCTGGGAACCAGGCTGAGTGGCCTCAAACCCCCCGTTGGATCAGACC 1560 Qy 1561 CTCCTGTGGGCAGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAACCAA 1620	RESULT. 12 ARX90370 standard; CINA; 1630 BP. XX ARX90370 standard; CINA; 1630 BP. XX ARX90370 standard; CINA; 1630 BP. XX Human secreted/transmembrane protein CDNA, #170. XX Human secreted/transmembrane; signal peptide; XX Human secreted/transmembrane; signal peptide; XX Human secreted/transmembrane; signal peptide; XX Homo saplens. Homo 1.200.1997; 970.200.0093259. RX Homo 1.200.1997; 970.200.0093259. RX Homo 1.200.1997; 970.200.0093218. RX Homo 1.200.1997; 970.20
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New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes.
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Fong S, Gerber H, Gerritsen ME, Goddard A,
Gurney AL, Kljavin IJ, Napier MA, Pan J,
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98US-0089598P.
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Ferrara N, Fong S, C
Grimaldi JC, Gurney P
Roy MA, Stewart TA,
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P-PSDB; ABU60611.
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Zhang
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Godowski PJ; Paoni NF; Wood WI; Eaton

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that

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molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The sequences presented in ABX90083-ABX90468 are the genes encoding, the primers amplifying and the probes detecting the PRO polymucleotides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at ö 180 180 240 240 300 300 360 120 120 360 420 420 480 480 540 540 900 600 9 099 720 720 780 9 9 TIGGATITIGAAAGTIGAGAGCAGCATGTITIGCCCCACTGAAACTCCTGCTGCTGCCAGTG TTCAAGATAGACTGGGACCTCTGTCACCAGGAGCACGCCAAGGACGATATGTGCTATAC 1 CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC 61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCCTGCTGCCAGTG TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC CATGTGGGTGATTCAGCTCTGATGGGATGTTTTTCCAGAGGCACAGAAGACAAATGTATA CATGTGGGTGATTCAGCTCTGATGGGATGTTTTCCAGAGCACAGAAGACAATGTATA TTCAAGATAGACTGGACTCTGTCACCAGGAGGAGGCCCAAGGACGAATATGTGCTATAC TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGG cecrceaerecaecrereseaaarrreaerecarrecerecereserecrerere TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGAGTCAGATGAGGAACTAC GACATCTTATGCAATGATGGCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA GACATCTTATGCAATGATGGCTCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGACCAGGTGTTCAAGAAGGCGGTGGTA ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGTA ATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTT ATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTT TCAGGACGCCGCCAAAGGAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT TCAGGACGCGCGCAAAGGAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT GIGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATT Grégadiaciccadascrégéeccacirccagaarcerergaaccrégrégéesearr TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGGAAACTAC for linking a bioactive .. Length 1630; Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other; Indels DB 7; 0 ; Query Match 100.0%; Score 1630; Best Local Similarity 100.0%; Pred. No. 0; Matches 1630; Conservative 0; Mismatches specifically bind to the PRO polypeptide, seqdata.uspto.gov/sequence.html 61 121 241 121 181 181 241 301 301 361 361 421 421 481 481 541 541 601 601 661 721 661 8 $\frac{1}{2}$ $\frac{1}{2}$ ठ g 셤 ò d ð g ò D δ q g g δ ò ŏ g ò g ò Q δ

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Human; PRO polypeptide; secreted and transmembrane protein;

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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ACA66841-ACA66962 represent cDNA sequences encoding the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in sequata.uspto.gov/psipsDIDEntry.html
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anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or the full length coding sequence of any these 122 nucleotide sequences. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour) in a mammal, for stimulating the release of TNF-alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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AGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGG 1500 or lung tumour; Wood WI; New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis CTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAACCAA **ACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCCGTTGGATCAGACC** Human, secreted and transmembrane protein, PRO; cytostatic, antiarthritic, osteopathic, gene therapy, INF-Agonist-Alpha, chondrocyte stimulator, pericyte stimulator, fibroblast modulator, pharmaceutical, diagnostic, biosensor, bioreactor, tumour, lung tu colon tumour, breast tumour, prostate tumour, rectal tumour, liver tumour, bone disorder, cartilage disorder, sports injury, PJ; Goddard A, Godung. Novel human secreted and transmembrane protein PRO1387 cDNA Gerritsen ME, Goddard Smith V, Stephan JF,

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cells, for stimulating proliferation of pericyte cells, or for modulating normal human dermal fibroblast proliferation. The PRO nucleic acid or polypeptide is also useful for treating tumours or various bone and/or cartilage disorders (e.g. sports injuries or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This sequence encodes a novel human secreted and transmembrane PRO
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       Homo sapiens
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bloactive molecules to cells expressing PRO polypeptides, for modulating concluding agonists or antagonists. The polynucleotide sequences concoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, to construct hybridisation probes for mapping the gene which encodes the PRO polypeptide, and for the generic analysis of individuals with genetic disorders, in gene therapy, for chromosome conduction, as chromosome markers, and for generating probes for polypeptide of the invention. Note: The sequence encodes a human PRO polypeptide of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
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Paoni NF;
Wood WI;
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DB 7; Length 1630;

Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

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qa	1561 CTCCTGTGGGCAGGGTTCTTAGTGGATTACTGGGAAGAATCAGAGTAAAAACCAA 1620
ογ	1621 CCCAAATCAA 1630
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Sequence 730, App
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Patent No. 6602667

GENERAL INFORMATION:

APPLICANT: Walker, Michael G.

APPLICANT: Wolkmuth, Wayne

TITLE OF INVENTION: Inflammation-Associated Polynucleotides

FILE REFERENCE: PB-0006-1 CIP

CURRENT APPLICATION NUMBER: US/09/855,323

CURRENT FILING DATE: 2001-05-14

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PERL Program

SEQ ID NO 11

LENGTH: 1751
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4 US-09-430-503-31

3 US-08-928-383B-1

3 US-09-272-496-1

4 US-09-276-594-730

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1 US-08-257-073-10

4 US-09-820-002-3

1 US-08-416-478A-5

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2 US-08-920-002-3

1 US-08-916-421B-1

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Matches 1622; Conservative
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ORGANISM: Homo sapiens
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Db 1548 GGAGGAACAGGCCTGAGGGGAGGACATGGACTTGGCCTCTGGAGTGGGACTG 1 Oy 1507 GCCCTGGAACCAGGCTGAGTGGCTCAAACCCCCGTTGGATCAGACCTCCTG 1 1608 GCCCTGGGAACCAGGCTGAGTGGCTCAAACCCCCGTTGGATCAGACCTTCTG 1 Oy 1567 TGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATCAGACCTCCTG 1 Db 1668 TGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAACCCAAA 1 1677 TCA 1629 Db 1728 TCA 1730	RESULT 2 US-09-656-952-18 i Sequence 18, Application US/09656952 j Patent No. 6444443 ; GENERAL INFORMATION: j APPLICANT: Gabor Jarai et al. rITLE OF INVENTION: No. 6444443el Gene FILE REFERENCE: 4-31440Pl/N1/HO 29 CURRENT FILING DATE: 2000-09-07 NUMBER OF SEQ ID NOS: 20 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 18 LENGTH: 1561 TYPE: DNA ORGANISM: Homo sapiens US-09-656-952-18	Query Match Best Local Similarity 99.5%; Pred. No. 0; Matches 1550; Conservative 0; Mismatches 7; Indels 1; Gaps Qy 44 CCTGGGTGCTCTTCATCTTGGATTTGAAGTTGAGGCATGTTTTGCCCACTGAAAC 1 Db 2 CCCTTGTGCTCTTCATCTTGGATTATTCCTTGGGCATGTTTTGCCCACTGAAAC 6 Qy 104 TCATCCTGCTGCAGTGTTACTGGATTATTCCTTGGGCCTGAATGATTTTCCC 1	
2y 367 TTATGCAATGATGGCTCTCCTGCTCCAAGATGTGCAAGAGCTGACCAGGGAACCTAT 426 [2y 607 CGGCGCGCAAAGGAGGATTGTATTTCGTTACTACCACAAACTCAGGATGTCTGTGGAG 666 10 11<	948 GAGCCTCGAACACTGGTGACCCCGGCAGCCTGAGGCCTCTGGTCTTGGGTGATATAGGTGATATAGGGTGATATAGGGTGATATAGGGTGATAGGGTGATAGGGTGATAGGGTGATAGGGTGATAGGGTGATAGGGTGATAGGGGAATTGTCGGGAATTGTCTGTGGCAATCCTGCTGCTCCCTGTTCTGATAGGGTTCAGGGAATTCTTGTGGGAATTGTCTGTGAAGGTTCAGTGAATTCTACAGTGAAGAGAGAAGAGAAGAAGAATAGAAATAGAAATTCTACAGTCTTGGTGAAGGTTCAGTGAAGATTCTACAGTCTTGGTGAAGGTGAAGGTTCAGTGAAGATCTTGGTGAAGATCTAGAAAAACCCTGCCATTTTGAAAGATGTGAAGATGTGAAGATGTGAAGAAAAACCCTGCCATTTTGAAAGATGTGAAGATGTGAAAAAACCCTGCCATTTTGAAAGATGTGAAATAGAAAAAACCCTGCCATTTTGAAAGATGTGAAATATAGAAAAAACCCTGCCATTTTGAAAGATGTGAAATATAGAAAAAACCCTGCCATTTTGAAAGATGTGAAAAAAAA	

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<pre>; Patent No. 6444443 ; GENERAL INFORMATION: ; APPLICANT: Gabor Jarai et al. ; TITLE OF INVENTION: No. 6444443el Gene ; FILE REFERENCE: 4-31440Pl/N1/HO 29 ; CURRENT APPLICATION NUMBER: US/09/656,952 ; CURRENT FILING DATE: 2000-09-07 ; SOFTWARE: Patentin Ver. 2.1 ; SOFTWARE: Patentin Ver. 2.1 ; SQ ID NO 17 ; LENGTH: 1591 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-656-952-17</pre>	Query Match Best Local 5 Matches 1550 Y 44	104 TCATCCTGCTGCCAGTGTTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCC 16	122 CGCCTGAGCTAACAGTCCATGTGGGTGATTCAGCTCTGATGGGATGTGTTTTCCAGAGCA 18 224 CAGAAGACAAATGTATATTCAAGATAGACTGACCTCTGTCACCAGGAGCACGCCAAGG 28	QY 284 ACGARTATGTGCTATTACTCCAATCTCAGTGTGCCTATTGGGCGTTCCAGAACC 343	404 AAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGT 46	422 TCAGGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCCAAAGAGCTCATGGTCCTTG 4 524 TGGGTGGATTGATTCAGATGGGATGTGTTTTCCAGAGCCACAGAAGTGAACACGTGACCA 5	QY 584 AGGTAGAATGGATTTTCAGGACGCGCGAAAGGAGAGATTGTATTTCGTTACTACC 643	Qy 704 ACCTGGTGGGGACATTTTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGAGT 763 Db	
Qy 584 AGGTAGAATGGATATTTCAGGACGGCGCAAAGGAGGAGATTGTATTTCGTTACTACC 643 bb 542 AGGTAGAATGGATATTTTCAGGACGCGCGCAAAGGAGGAGATTGTATTTCGTTACTACC 601 cv 644 ACAAACTCAGGATGTCTGTGGACGCGCGCGCGCAAAGGAGGAGATTGTATTTCGTTACTACC 601 cv 602 ACAAACTCAGGATGTCTGCGAGGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGA 661 cv 704 ACCTGGTGGGGACATTTTCCGCAATGACGTTCCATCATGCTTCAAGGAGTGAGGGAGT 763 cctGGTGGGGGACATTTTCCGCAATGACGTTCCATCATGCTTCAAGGAGTGAGGAGT 763 cctGGTGGGGGACATTTTCCGCAATGACGGTTCCATCATCATGCTTCAAGGAGTGT 721 cc ACCTGGTGGGGGACATTTTCCGCAATGACGTTCCATCATCATCATGCTTCAAGGAGTGT 721 cc ACGTGGTGGGGGACATTTTCCGCAATGACGTTCCATCATCATCATCATCATCATCAAGAAACCA 823 cc ACGATGGAGGAAACTACACCTGCAGTATCCACCTTAGGAACTTCCAAGAAAACCA 823			1004 ATTCTACAGTCTTGGTGAAGACACGAAGAAGACTAATCCAGAGATAAAGAAAAACCT 106	DD	1142 TTTGGCCTTCTCTGAGGTCAGATCGGAACAACTCACTTGAAAAAAAGTCAGGTGGGGGAA 120 1244 TGCCAAAAACACAACCAAGCCTTTTGAGAAGAATGGAGAGTCCCTTCATCATCTCAGCAGGGT 130	1304 GGAGACTCTCTCTGTGTGTCTGGGCCACTCTACCAGTGATTTCAGACTCCCGCTCT 136	Db 1322 CCCAGCTGTCCTCTGTTTGGTCAATACACTGAAGATTTGGAGGCC 1381 Qy 1424 TGGCAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGCAGGAGCATGGAC 1483		RESULT 3 US-09-656-952-17 ; Sequence 17, Application US/09656952

RESULT 3 US-09-656-952-17 ; Sequence 17, Application US/09656952

824 TIGIGCIGCALGICAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGC 883

Gaps

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Score 1483.8;
Pred. No. 0;
0; Mismatches
Query Match
Best Local Similarity 97.5%;
Matches 1550; Conservative
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                          CTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGGAATTGTCTGTGCCACAATCC
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Patent No. 6444443;
GENERAL INFORMATION:
APPLICANT: Gabor Jarai et al.
TITLE OF INVENTION: No. 6444443e1 Gene;
FILE REFERENCE: 4-31440p1/N1/HO 29;
CURRENT APPLICATION NUMBER: US/09/656,952;
CURRENT FILING DATE: 2000-09-07;
NUMBER OF SEQ ID NOS: 20;
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1592;
TYPE: DNA
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Pred. No. 0;
0; Mismatches
    REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                           0S
                                                                                                                                                                                                                                                                                   Query Match 73.3%;
Best Local Similarity 99.9%;
Matches 1195; Conservative
                                                                                                                                                                             ; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SPLNFET01
; CLONE: 027756
US-09-023-655-131
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1202 AACTCACTTGAAAAAAAGTCAGGTGGGGAATGCCAAAAACACAGGAAGCCTTTTGAGAA
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                                                                                      CACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
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US-09-023-655-131
; Sequence 131, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: COMPOSITION FOR THE DETI:
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
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                                                1334 ACTCTACCAGTGATTTCAGACTCCCGCTCTCCCAGCTGTCCTCCTGTCTCATTGTTTGGT
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                                                                             901 AcreraceAgrearricaGacreceGerereceAgerGreerGreerGreer
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APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOY, John M.
APPLICANT: Racie, Lisa M.
APPLICANT: Racie, Lisa M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Bvans, Cheryl
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,680
FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: MA COUNTRY: U.S.A. ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:

NAME: Springer, Suzanne A.

REGISTRATION NUMBER: P-41,323

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8284

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1024 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08867680
Patent No. 5958726
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                      62 TIGAAAGTIGAGAGCAGCATGTITIGCCCACTGAAACTCATCCTGCTGCCAGTGTTACTG
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                                                                                                    7 GAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTTGGAT
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Length 1024;
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TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT FILING DATE: 12000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/084,121
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR PILING DATE: 1998-04-13
PRIOR PILING DATE: 1998-04-13
                                                  Indels
Score 609.8; DB 2;
Pred. No. 1.3e-194;
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                                                  0; Mismatches
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  Query Match
Best Local Similarity 99.7
Matches 611; Conservative
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; OTHER INFORMATION: n=a, g, c or US-09-663-600A-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1133._1138
NAME/KEY: polyA_site
LOCATION: 1146._1158
NAME/KEY: misc_feature
LOCATION: 652
                                                      US-09-663-600A-144
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Pred. No. 9.4e-153;
3; Mismatches 2; Indels 1;
                                                                                                                                 FEATURE:
NAME/KEY: sig peptide
LOCATION: 214.339
OTHER INFORMATION: Won Heijne matrix
OTHER INFORMATION: Score 6.0999990463257
OTHER INFORMATION: seq AllLLQSQCAYWA/LP
NAME/KEY: polyA_signal
LOCATION: 1133.1138
NAME/KEY: misc_feature
LOCATION: 840.368
OTHER INFORMATION: homology
OTHER INFORMATION: id :H64717
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 850.368
OTHER INFORMATION: id :H65208
OTHER INFORMATION: id :H65208
OTHER INFORMATION: id :H65208
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 852.
COTHER INFORMATION: id :H65208
OTHER INFORMATION: id :H65208
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 652

COTHER INFORMATION: n=a, g, c or t
US-09-663-600A-50
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 50
LENGTH: 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIGCTICCAGAGGAGCCCAAAG 515
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98.8%;
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Best Local Similarity 98.89
Matches 496; Conservative
                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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126 186 GGTGATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAG 246 ATAGACTGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTAC 306 TCCAAICTCAGIGGCCTAITGGGCGCTTCCAGAACCGCGTACACTIGAIGGGGGGACAIC 366 254 ATAGACTGGACTCTGTCACCAGAGAGAGCACGCCAAGGACGAATATGTGCTATACTATTAC 313 314 recalitricadiorectalicececriceagaaceceracaricaregessacare 373 367 TTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTAT 426 74 GATTATTCCTTGGGCCTGAATGATTTCCCCGCCTGAGCTAACAGTCCATGTG 15 GACTGCAGCTGTGGGAGATTTCAGTGCATTGCCTCCCTGGGTGCTCTTCATCTTGGAT TIGAAAGIIIGAGGAGCAIGIIIIIGCCCACIGAAACICAICCIGCIGCCAGIGIIACIG 7 GAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCTCCCTGGGTGCTCTTCATCTTGGAT 1; Gaps Query Match 29.8%; Score 485.6; DB 4; Length 1158; Best Local Similarity 98.8%; Pred. No. 9.4e-153; Matches 496; Conservative 3; Mismatches 2; Indels 1; Sequence 144 Application US/09663600A; Patent No. 65730B; Patent No. 65730B; Patent No. 65730B; Patent No. 65730B; GENERAL INFORMATION:

APPLICANT: Dunas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Duclert, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS; FILB REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A; CURRENT APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: PATENT.PM

Mon Oct

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1092 ACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAACAACAAGTGAAAA 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHOTITLE OF INVENTION: DIAGNOSIS OF LUNG CANCELLE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FARESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-736-457-1549; Sequence 1549, Application US/09736457; Patent No. 6509448; GENERAL INFORMATION:
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; Patent No. 6504010
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Bangur, Chaitanya S.
Lodes, Michael A.
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Bangur, Chaitanya
Lodes, Michael A.
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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Vedvick, Tom
Carter, Darrick
Retter, Marc
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Best Local Similarity
Matches 91; Conserv
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US-09-702-705-1549
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                                                                           374 TTATGCAATGACTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTAT 433
                                                       ATCTGTGAAATCCGCCTCAAAGGGGAGAGACCCAGGTGTTCAAGAAGGCGGTGGTACTGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30472/114 IMMU
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PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                           487 GIGCITCCAGAGGAGCCCAAAG 508
                                                                                                                                                           494 GTGCTTCCAGAGGAGCCCAAAG 515
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TYPE: nucleic acid
STRANDEDNESS: single
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.larity 52.0%; Pred. No. 0.0035;
Conservative 0; Mismatches 84; Indels
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FILING DATE:
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US-08-416-478A-1
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APPLICANT:
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APPLICANT:
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Matches 9
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APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1549
LENGTH: 438
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Machael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
WUMBER OF SEQ ID NOS: 1668
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                      Score 40.6; DB 4; Length 438;
Pred. No. 0.0035;
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Pred. No. 0.0035;
0; Mismatches 84;
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-614-124B-1549
; Sequence 1549, Application US/09614124B
; Patent No. 6630574
                                                                                                                                                                                                                                                                                                                     2.5%;
llarity 52.0%;
Conservative
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APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya
APPLICANT: Lodes, Michael A.
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Best Local Similarity 52.0°
Matches 91; Conservative
                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-1549
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US-09-614-124B-1549
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Best Local Similarity
Matches 91; Conserv
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Sequence 1, Application US/08416478A
Sequence 1, Application US/08416478A
Sequence 1, Application US/08416478A
Sequence 1, Application Sequence 1, Applicant Sequence 1
APPLICANT: Hercend, Thierry
APPLICANT: Triebel, Frederic
TITLE OF INVENTION: Lymphocytes, DNA Sequences Encoding These Proteins And
TITLE OF INVENTION: Their Pharmaceutical And Biological Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
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262 CCCAAATCCTTTGGGTCACCTGGATCCCTGGGGAAGCTGCTTTGTGAGGTGACTC 316
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Pred. No. 0.0035;
0; Mismatches 84; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,478A
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS ITITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UMBER: US/08/416,478A
04-APR-1995
                                                                                                                                Sequence 1549, Application US/09671325 Patent No. 6667154
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IBM PC compatible
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Bangur, Chaitanya
Lodes, Michael A.
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Vedvick, Tom
Carter, Darrick
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Mannion, Jane
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MEDIUM TYPE: Floppy
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ORGANISM: Homo sapien
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STATE: D.C.
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NEW PROTEINS PRODUCED BY HUMAN
LYMPHOCYTES, DNA SEQUENCES ENCODING THESE PROTEINS AND
THEIR PHARMACEUTICAL AND BIOLOGICAL USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,988B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/416,478
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: A95
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GENERAL INFORMATION:
APPLICANT: Hercend, Thierry
APPLICANT: Tribel, Frederic
TITLE OF INVENTION: LYMPHOCYTES, DNA SEQUENCES I
TITLE OF INVENTION: THEIR PHARMACEUTICAL AND BIC
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,644
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: HERCEND=1A
TELECOMMUNICATION INFORMATION:
TELEFPHONE: (202) 628-5197
TELEFPAX: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1871 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; LOCATION:
US-08-416-478A-1
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                                          REFERENCE/DOCKET NUMBER: 37,971
REFERENCE/DOCKET NUMBER: HERCEND=1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                      LENGTH: 1871 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                       CDS
231..1724
                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                       TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lin
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; LOCATION:
US-08-474-988B-1
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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October 1, 2004, 19:38:55; Search time 10107 Seconds (without alignments) 6990.120 Million cell updates/sec
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OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1630
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Perfect score:
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                           Run on:
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38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

C. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1630 100.0 1630 6 AX32655 5 Gague 1630 100.0 1630 6 AX36435 5 AX36435 5 Gague 1630 100.0 1630 6 AX36435 5 AX36435 5 Gague 1630 100.0 1630 6 AX4643842 AX366435 5 Gague 1630 100.0 1630 6 AX464384 AX463534 5 Gague 1630 100.0 1630 6 AX464386 AX463534 AX46354 AX46354 AX46354 AX46354 AX46364 AX46364 AX46364 AX46364 AX46364 AX46364 AX46364 AX46364 AX66364 A	Result		Query				
1630 100.0 1630 6 AX352655 Seq 1630 100.0 1630 6 AX358942 AX358942 AX358942 Seq 1630 100.0 1630 6 AX358942 AX45849 Seq 1630 100.0 1630 6 AX46438 AX46438 Seq 1630 100.0 1630 6 AX46438 AX46438 Seq 1630 100.0 1630 6 AX46438 AX46438 Seq 1631 100.0 1630 6 AX46438 AX46438 Seq 1631 100.0 1630 6 AX46438 AX491126 Seq 1631 100.0 1630 6 AX491126 AX491126 Seq 1621.4 99.5 1751 6 BD248693 Info 1621.4 99.5 1751 6 AX33304 AX493104 Seq 1621.4 99.5 1751 6 AX33304 AX493104 Seq 1621.4 99.5 1751 6 AX33304 AX493104 AX493104 Seq 1631.9 92.5 1551 6 AX33304 AX493104 AX33302 Seq 1641.8 92.5 1551 6 AX33304 AX49302 AX493304 AX493304 1641.8 92.5 1551 6 AX33302 AX493302 Seq 1641.8 92.5 1559 6 AX83302 AX69309 Seq 1641.8 91.1 1599 6 AX693499 AX693304 AX693304 AX693304 1641.8 91.1 1599 6 AX693499 AX69349 Seq 1641.8 91.1 1599 6 AX693499 AX693494 Seq 1641.8 91.1 1590 6 AX693499 AX693494 Seq 1641.8 91.1 1590 6 AX693499 AX693494 Seq 1641.8 91.1 1590 6 AX693499 AX693494 Seq 1641.8 91.1 1620 1820 6 AX693499 AX693494 Seq 1641.8 91.1 1620 6 AX69349 AX693494 Seq 1641.8 91.1 1620 6 AX69349 AX693494 Seq 1641.8 91.1 1624 6 AX69349 AX69349 Seq 1641.8 91.1 1624 6 AX69349 Seq 1641.8 91.1 91.1 Sec BD068990 AX69990 BD068990 AX69990	No.	Score	Match	Lengt]	8	QI	scripti
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1630 100.0 1630 6 AX362435 AX462435 Seq. 1630 100.0 1630 6 AX4636445 AX463648 Seq. 1630 100.0 1630 6 AX46386 AX464386 Seq. 1630 100.0 1630 6 AX49126 AX491126 AX491126 Seq. 1621.4 99.5 1751 6 AX23344 AX347306 AX347307 Seq. 1621.4 99.5 1751 6 AX25785 AX347307 AX347308 AX347308 AX347308 AX47308 AX47308 AX47308 AX47308 AX47309 AX47309 AX47309 AX47309 AX47309 AX47309 AX47309 AX47709 AX609447 AX47709 AX609447 AX47709 AX609447 AX47709 AX609447 AX609447 AX47709 AX609447 AX6094	(1)	63	00	ĩ	9	AX358942	58942 Sequence
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ALIGNMENTS

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RESULT 1 AR252655 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding Craniata, Vertebrata, Euteleostomi; Catarrhini, Hominidae, Homo. Acachesconsesacoasconsecusasconsasconoaacococonosasconos ACACTGGCCCTGGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCCGGTTGGATCAGACC GAAGGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAAA CCAAGTGAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCTTCTGAGG CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTGAGG TCAGATCGGAACAACTCACTTGAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA CICATIGITIGGICAATACACIGAAGAIGGAGAATITIGGAGCCIGGCAGAGAGIGGAC AGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGG 961 ATATTGATCGTGAAGAGACCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGGTG GAAGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAA GCCTTTTGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCCTGTG TGTGTCCTGGGCCACTCTACCAGTGATTTCAGACTCCCGCTCTCCCAGCTGTCCTCCTGT AAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCTGCCATTTTGAAAGATGT linear the ...
Patent: WO 0193500.
Genentech Inc. (US)
Location/Qualifiers
1. 1630
/organism="Homo sapiens"
/mol_type="unassigned DNA" DNA AX358942 1630 bp Sequence 195 from Patent WO0193983. AX358942 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; AX358942.1 GI:18675372 Homo sapiens (human) CCCAAATCAA 1630 1621 CCCAAATCAA 1630 1141 1201 1261 1381 1381 1441 1501 1501 1621 1021 1081 1201 1321 1321 1081 1141 1261 1021 source ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 2 AX358942 LOCUS DEFINITION

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Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Genentech Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CGGCTCGAGTGCAGTGCATTGCCTCCCTGGGTGCTCTTCATC 60 1 CGGCTCGAGTGCTGTGGGGAGATTTCAGTGCATTGCCTCCCTGGGTGCTCTTCATC 60 CGGCTCGAGTGCTGGAGAGATTTCGCCACTGGAAACTCATCATC 60 CGGCTCGAGTGTTGAAAGTTGAGAGAGAGATTTGCCCACTGAAACTCGTGCTGCTGCTGCTGCTGCTGCTGCTGGGGTG 120 CGGTTGAAAGTTGAAAGTTTGCAATGATTTGCCCACTGAAACTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	121 TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC 180 181 CATGTGGGTGATTCCTTGATGGGATGTTTTCCAGAGCACAGAAGACAAATGTATA 240	241 TICAAGATAGACTGGACTCTGTCACCAGGAGCACGCCAAGGACGAATATGTGCTATAC 300 301 TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGG 360 [ATGGGATGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTT	TCAGGACGCGCGCAAAGGAGATTGTATTTCGTTACTACCAAACTCAGGATGTCT TCAGGACGCGCGCAAAGGAGATTGTATTTCGTTACTACCAAACTCAGGATGTCT GTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGGAACCTGGTGGGGGACATT	721 TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGGAAACTAC 780	ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAAGAAACCATTGTGCTGCATGTCAGC CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTTTTGGGTGTT CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGT CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTTAAGGTTTTTTTT		961 ATATTGATCGTGAAGACCTGTGGAATAAGAGTTCAGTGAATTCTACAGTCTTGGTG 1020

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Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Wood,W.L. and Zhang,Z.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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        GCCTTTTGAGAAGAATGGAGACTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTG
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Patent: WO 0200690-A 233 03-JAN-2002;
Genentech, Inc. (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 233 from Patent WO0200690.
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Best Local Similarity 100.0%; Pred. No. 0; Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC 60	}	TIGGATITGAAAGITGAGAGCAGCATGITTTGCCCACTGAAACTCATCCTGCTGCCAGTG 12	12	TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC 18	TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC 18	181 CATGTGGGTGATTCAGCTCTGATGGGATGTTTTTCCAGAGCACAGAAGACAATGTATA 240 	TTCAAGATAGACTGGAC		301 TATTACTCCAATCTCAGTGTGCCTATTGGCGCTTCCAGAACCGCGTACACTTGATGGGG 360	301 TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACGGGGTACACTTGATGGGGG 360	GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA 42	361 ĠACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA 420	ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTA 48	CCGCCTCAAAGGGAAGCCAGGTGTTCAAGAAGGCGGTGGTA 48	481 CTGCATGTGCTTCCAGAGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGG	A THE AT ACCUMENT OF THE PROPERTY OF THE PROPE	ATGGGATGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTT 60	601 TCAGGACGGCGCAAAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT 660	601 TCAGGACGGCGCAAAAGGAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT 660	661 GTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATT 720	cidodocaciticcadaarcororaaaccroorogodo	721 TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGGGTCAGATGGAGGAACTAC 780	TICCGCAAIGACGGIICCAICAIGCIIICAAGGAAGIGAGGAGGACICAGAIGAGAAGAAGAAAATAACIAAAAAAAAAA	r 41	CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGAGCCTCTGGTCTTGGGTGT 90	841 CCGGAAGACCTCGAACACTGGTGACCCCCGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGT 900	901 AATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTGCTCCTGTTCTG 960	901 AATCAGTIGATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTCCTGTTCTG 960	961 ATATTGATCGTGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGGTG 1020	21
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aryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
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rk,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
d,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
dens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
nson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
dard,A., Wood,W.I. and Godowski,P.
Secreted Protein Discovery Initiative (SPDI), a Large-Scale
ort to Identify Novel Human Secreted and Transmembrane Proteins:
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ed (01-AUG-2003) Department of Bioinformatics, Genentech,

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I (bases 1 to 1751)

RS Walker,M.G., Volkmuth,W. and Klingler,T.M.

Inflammation-associated genes
Inflammation-All
PD TO 2002530077-All
PD 17-SEP-2002
PF 04-NOV-1999 US 09/195292
PF 18-NOV-1999 US 09/195292
PF 18-NOV-1999 US 09/195292
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PC A61R37/02
CC Incyte ID No.: 3507924CB1
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             BD248693.1 GI;33058463
BD248693.1 GI;33058463
JP 2002530077-A/11.
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism='Homo sapiens
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Mammalia; Eutheria; Primates; Catarrh
1 (bases 1 to 1635)
Foster, J.S. and Gurney, A.L.
Direct Submission
Submitted (02-AUG-2002) Molecular Bic
South San Francisco, CA 94080, USA
Location/Qualifiers
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1. .1635
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Homo sapiens adhesion molecule A

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QY 1570 GCAGGGTTCTTAGTGGATGAGTTACTGGGAAGATCAGAGATAAAAACCAACC	RESULT 12 AR225785 LOCUS LOCUS DEFINITION Sequence 18 from patent US 6444443. ACCESSION AR225785 VERSION AR225785.1 GI:27263889 VERYORDS SOURCE ORGANISM Unknown. ORGANISM Unknown. ACRESERENCE 1 (bases 1 to 1561) AUTILE Gene JOURNAL Patent: US 6444443-A 18 03-SEP-2002; TITLE JOURNAL Patent: US 6444443-A 18 03-SEP-2002; FEATURES SOURCE JOCATION/Qualifiers I . 1561 //organism="unknown" //organism="unknown" //mol_type="genomic DNA"	Query Match 94.2%; Score 1534.8; DB 6; Length 1561; Best Local Similarity 99.5%; Pred. No. 0; 7; Indels 1; 1; Matches 1550; Conservative 0; Mismatches 7; Indels 1; 1; Qy 44 CCTGGGTGCTCTTCATCTTGAATTTGAAAGTTGAGAGCAGCATGTTTGCCCACTGAAAC 103 1 1 Db 2 CCCTTGTGCTCTTCATCTTGGATTATTCCTTGGGCCTGAATGTTTGCCACTGAAAC 61 0 Qy 104 TCATCCTGCCGGTGTTACTGGATTATTCCTTGGGCCTGAATGTTTCC 163 1 Pb 62 TCATCCTGCCGGTGTTACTGGATTATACCTTGGGCCTGAATGTTTCCC 121	Oy 164 CGCCTGAGCTAACAGTCCATGTGGGTGATTCAGCTCTGATGGGATGTTTTCCAGAGCA 223	3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Qy 464 TCAAGAAGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCCAAAGAGCTCATGGTCCATG 523

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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                      Jarai, G. and Yousefi, S.

Novel gene
Patent: WO 0187938-A 18 22-NOV-2001;
Location/Qualifiers
1. .1561
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                  Score 1534.8;
Pred. No. 0;
0; Mismatches
                                                                                                                                                   Query Match 94.2%;
Best Local Similarity 99.5%;
Matches 1550; Conservative (
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

El (bases 1 to 1649)

El Hillman, J.L., Bandman, O., Lal, P., Yue, H., Reddy, R., Tang, T.Y.,

Gerstin, E.H., Patterson, C., Baughn, M.R., Azimzai, Y. and Lu, D.A.M.

Human transcriptional regulator molecules

INCYTE PHARMACEUTICALS INC

OS Homo sapiens (human)

EN JP 2002513554-A/47

ED 14-MAY-2002

FF 04-MAY-1999 JP 2000547113

PR 05-MAY-1999 US 60/084254,07-AUG-1998 US 60/095827 PR

02-OCT-1998 US 60/102745
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CTCTGGTCTTGGGTGATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCC
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Human transcriptional regulator mc BD209975
BD209975.1 GI:33019745
JP 2002513554-A/47.
Homo sapiens (human)
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Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                  CCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATC
                                                                                                   CTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAGTG
                                                                                                                                                   AATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAACCC
                                                                                                                                                                                                    TGCCATTTTGAAAGATGTGAAGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAG
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                                                     CCTCTGGTCTTGGGTGGTAATCAGTTGGTGATTGTGGGAATTGTCTGTGCCACAATC
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Sequence 152 from Patent EP1347046.
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C12N15/09, A61K38/00, A61K45/00, A61P35/00, A61P37/02, A61P43/00, C07K14/47,
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PC C12N15/09, A61K38/00, A61K45/00, A61P35/00, A61P37/02, A61P43/00
PC C07K14/47,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/68//C12P21/
JENNIFER L HILLMAN, OLGA BANDMAN, PREETI LAL, HENRY YUE, ROOPA
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Full-length cDNA sequences
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Research Association for Biotechnology (J)
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AY420493
Pan troglodytes HCM7242 gene, VIRTUAL TRANSCRIPT, partial sequence,
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1 (bases 1 to 911)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
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Science 302 (5652), 1960-1963 (2003)
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BI767696
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A1185656 qe65c08.x CD472358 LeukoS6 5 AA043360 zk62e11.5

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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence as made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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Contact: Genoscope.
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Contact: Genoscope. Centre National de Sequencage
Genoscope. Centre National
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6071.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1AJ002ZD01NP1&cluster=6071.r. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1AJ002ZD01NP1.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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FEATURES Location/Qualifiers 11054 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DL002YK09" /cell_type="B_CELLS (RAMOS CELL LINE) COT 25-NORMALIZED" /cell_line="RAMOS CELL LINE" /clone="Lamo sapiens B_CELLS (RAMOS CELL LINE) COT 25-NORMALIZED" /clone="lamo sapiens B_CELLS (RAMOS CELL LINE) COT	Query Match Best Local Similarity 92.5%; Pred. No. 1.8e-212; Matches 910; Conservative 13; Mismatches 55; Indels 6; Gaps 4; Qy 21 GGAGATTTCAGTGCATTGCCTCCCTGGGTGCTCTTCATCTTGAAAGTTGAAAGTTGAAAGTTGAAAGTTGAAAGTTGAAAGTTGAAAGTTGAAAGTTGAAAAAGTTGAAAAAA		QY 141 CCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTGGGTGATTCAGCTCT 200	Qy 201 GATGGGATGTCTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGATAGACTGGACTCT 260	OY 261 GTCACCAGGAGGACGCCAAGGACGAATATGTGCTATACTACTACTACCAATCTCAGTGT 320	2y 321 GCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGGACATCTTATGCAATGATGG 380	CTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGAGAACCTATATCTGTGAAATCCG 44 CTCTCCTGCTCCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCG 48 ICAAAGGGGGAGGCCAGGTGATCAAGAAGGCTGACCTGATGTTTTTCTGTGAAATCCG 50 ICAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTTGCTTTTTTCCAGAGG 50 ICAAAGAGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTTGCTTTTTTCCAGAGG 60 CCAAAGAGGCTCATGTGGGTGGATTGATTCAGGATGTGTTTTTCCAGAG 60 CAAAAGAGAGCTCATGTGGGTGGATTGATTTTCAGGATGTTTTTCCAGAG 60 CAAAAGAGACCCATGTGGGTGGATTGATTTTCAGGATGTTTTTCCAGAG 60 CAAAAGAGAACCCAAAGTAGAATGGATTTTTCAGGATGTTTTTCCAGAG 60 CAAAAGTGAAACACGTGACCAAACTCAGGATGTTTTTCAGGAGTACTTTCCAGAGGT 60 CAATTGTATTTCGTTACTACCACAAACTCAGGATGTCTTTCCCAGAGCTG 728 CAATTGTATTTCGTTACTACCACAAACTCAGGATGTCTTTCCCCAGAGCTG 728 CACACTTCCAGAATCGTGAACCTGGTGGGAATGTTTTCCCCCAATGACGTTCCAT 74 CCCACTTCCAGAATCGTGAACCTGGTGGGGACATTTCCCCCAATGACGTTCCAT 74 CCCTTCAAGGAGTTGAACCTGGTGGGGGACATTTTCCGCAATGACGTTCCAT 74 CCCTTCAAGGAGTTGAACCTGGTGGGGGACATTTTCCGCAATGACGTTCCAT 74 CCCTTCAAGGAGTTGAACCTGGTGGGGGACATTTTCCCCCAATGACGTTCCAT 74 CCCTTCAAGGAGTTGAACCTGGTGGGGGACATTTTCCCCCAATGACGTTCCAT 74 CCCTTCAAGGAGTTGAACCTGGTGGGGGAAACTACCCCCGCAATGACGTTCCAT 74 CCCTTCAAGGAGTTGAAACCATGAGGAAACTACACCTGCCGTAATCCACCTAGG 848 CCCTTCAAGGAGTTCAAAAACCATTGTGCTCAATGACCCTGCAAAACCCCTGCAAACCCCTGCAAACCCCTGCAAACCCCTGCAAACCCCTGCAAACCCCTGCAAACCCCTGCAAACCCCTGCAAACCCCTGCAAACCCCTGCAAACCCCTGCAAACCCCTGCAAACCCCTCCAAACCCCTAAACCCTTCCAAACCCCTAAACCCTTCCAAACCCCTAAACCCTTCCAAACCCCTAAACCCTTCCAAACCCCTAAACCCCTAAACCCTTCCAAACCCTAAACCACTTCCAAACCCTAAACCCTAAACCACTTCCAAACCCTAAACCACTTCCAAACCCTAAACCACTTCCAAACCCTAAACCCTAAACCACTTCCAAACCCTAAACCCTAAACCCTAAACCCTAAACCCCTAAACCCTAAACCCCTAAACCCTAAACCCTAAACCCCTAAACCCTAAACCCTAAACCCTAAACCCTAAACCCCTAAACCAAACCCTAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAA
QY 959 TGATATTGATCGTGAAGAACCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGG 1018 Db 658 TGATATTGATCGTGAAGAACCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGG 599 QY 1019 TGAAGAACACGAAGAACATAATCCAGAGATAAAAAGAAAAACCTGCCATTTTGAAAGAT 1078 Db 598 TGAAGAACACGAAGAACTAATCCAGAGATAAAAAAAAAA	Qy 1199 GGTCAGATCGGAACAACTTCACTTGAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGC 1258	Db 358 AAGCCTTTTGAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGARACTCTCCTG 299 Qy 1319 TGTGTGTCCTGGGCCACTCTACCAGTGATTTCAGACTCCCGCTCTCCCAGCTGTCCTCCT 1378 Db 298 TGTGTGTCCTGGGCCACTCTACCAGTGATTTCAGACTCCCGCTCTCCCAGCTGTCCTCT 239	Qy 1379 GTCTCATTGTTAGTCAATACACTGAAGAATTTGGAGCCTGGCAGAGAGACTGG 1438 	Qy 1439 ACAGCTCTGGAGGAACAGGCCTGCTGAGGGAGGGAGGGAG	Oy 1499 GGACACTGGCCTGGGAACCAGGCTGAGCTGAGTGGCTCAAACCCCCCGTTGGATCAGA 1558 :	Qy 1559 CCCTCCTGTGGGCTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAA 1613 	RESULT 3 BX346274 BX3627 BX346274 BX3627 BX

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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Invitrogen. This sequence belongs to sequence cluster 6071.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DG006DB08QP1&cluster=6071.r. Contact:
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DG006DB08QP1.
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/tissue type="B CELLS (RAMOS CELL LINE)"
/cell line="RAMOS CELL LINE"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pcMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
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911 bp mRNA linear EST 15-MAY-2003
BX421455 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
clone CS0DG006YD16 5-PRIME, mRNA sequence.
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1 (bases 1 to 911)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                  GGAMCTGKGTGTTCAAGAAAACCATTGTGCTGCAGTGTCAGCCCGGRAGAG-CTCGAACAC
                                                TGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTG
                                                                  TGGGAATTGTCTGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGA
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Pred. No. 8.4e-212;
3; Mismatches 6; Indels 1;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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larity 98.8%;
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(bases 1 to 911)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence as made by sequencing genomic exons and ordering based on alignment.
                                                                                                                                                                                                                                                                                  ATGITTIGCCCACTGAAACTCATCCTGCTGCCAGTGTTACTGGATTATTCCTTGGGCCTG
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Pred. No. 1e-209;
0; Mismatches 82; Indels
                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                            /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                              /locus_tag="HCM7242"
                                                                                                                      Location/Qualifiers
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Best Local Similarity 91.0%;
Matches 829; Conservative
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6071.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAK046AB11NM1&cluster=6071.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAK046AB11NM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX414034 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA
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/cell line="RAMOS CELL LINE"
/cell line="RAMOS CELL LINE"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                   840
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1 (bases 1 to 915)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
CTGGTGTTCAAGAAACCATTGTGCTGCATGTCAGCCCGGAAGAGCCCTCGAACACTGGTG
                                                                                                                        781 ACCCCGGCAGCCCTGTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGA
                                                                                                                                                                                          ATTGTCTGTGCCACAATCCTGCTGCTCCTGTTCTGATATTGATCGTGAAGAGACCTGT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODG006YD16"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TGCAAGTCAGCCCGGAAGAGCCTCGAACACTGGTGGCCCCCGGCAGCCCTAAGGCCTCTGG
                                     TCCCTGTTCTGATATTGATCGTGAAGAGACCTGTGGAAATAAGAGTTCAGTGAATTCTA
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                                                                                                                                                                     TTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTACGGGGGGGTGATCG
                                                                                                                                                                                                                    AGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGC
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                                                                                                                                          AGGAAGAAGAACCAAGTGAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
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/lab host="DH10B"
/clone lib="NH10B"
/clone lib="NH10B"
/clone lib="NHH MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
pcMv-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; I
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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Tissue Procurement: Life Technologies, Lic.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov. j column: 24

High quality sequence stop: 699.

High quality sequence stop: 699.

Location/Qualifiers

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/organism="Homo sapiens"
/... ......mRNA."
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                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5753591"
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5226473"
/lab_host="DH10B"
/clone lib="NIH_MGC 120"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1:5 kb, insert size range 1-2:5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
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sapiens cDNA clone IMAGE:5226473 5',
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GAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCTGTGGAGTACTCCCAGAGC
                   ATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11569 row: o column: 18
High quality sequence start: 5
High quality sequence stop: 849.
Location/Qualifiers
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48.6%; Score 791.4; DB 12; Length 849;
Best Local Similarity 98.8%; Pred. No. 7.4e-200;
Matches 839; Conservative 0; Mismatches 6; Indels 4;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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BX346273
BX346273 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED Homo sapiens CDNA clone CSODL002YK08 3-PRIME, mRNA sequence.
BX346273
                                                                                                                                                 Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGAC 732

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Query Match
Best Local Similarity
Matches 782; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                            /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                        /cell type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
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/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                                                                                                                                      For
                                                                                                                                                                                 cgi-bin/cluster.cgi?seq=CSOAL002BF04NP1&cluster=6071.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOAL002BF04NP1.
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                                                              Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6071.r |
more information about this cluster, see
http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.4%; Score 739.8; DB 13; Length 1079; 96.2%; Pred. No. 5e-186; iive 7; Mismatches 21; Indels 3;
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL002YK08"
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/clone lib="NIH MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note:
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mRNA sequence.
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1 (bases 1 to 790)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can tound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11526 row: h column: 13
High quality sequence stop: 776.
Location/Qualifiers
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Pred. No. 8.3e-185;
0; Mismatches 5;
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this is a NIH_MGC Library.'
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              AAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCCTGCTGCCAGTGTTACTGGATT
                                                             ATTCAGCTCTGATGGGATGTTTTTCCAGAGCACAGAGACAAATGTATATTCAAGATAG
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758 bp mRNA linear EST 01-NOV-2002 UI-H-FTI-bht-e-06-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone CA306656 CA306656.1 GI:24469709 EST. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 758)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Homo sapiens (human) Homo sapiens RESULT 11 CA306656/c LOCUS VERSION KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS TITLE JOURNAL COMMENT ACCESSION

1367

lucation/Qualifiers
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| wol type="mRNA" |
| wol type="mRNA" |
| db xref="Laxon:9606" |
| /tissue_type="Avon:9606" |
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| /tissue_type="Avolar Macrophage" |
| /tissue_type="Adult" |
| /tissu cDNA Library preparation: Dr. M. Hunninghake, U of I cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD ۲; 1007 1067 1127 1187 1247 947 1307 640 700 580 460 400 340 TACAGTCTTGGTGAAGAACACGAAGAAGACACTAATCCAGAGATAAAAGAAAAACCCTGCCA GGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTGCT GCTCCCTGTTCTGATATTGATCGTGAAAGACCTGTGGAAATAAGAGTTCAGTGAATTC GCTCCCTGTTCTGATATTGATCGTGAAGAACCTGTGGAAATAAGAGTTCAGTGAATTC TACAGTCTTGGTGAAGAACACGAAGAAGACTAAATCCAGAGATAAAAGAAAAACCTGCCA TTTTGAAAGATGTGAAGGGGAGAACACATTTACTCCCCAATAATTGTACGGGAGGTGAT CGAGGAAGAAGCAAGTGAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTG TTNTGAAAGATGTGAAGGGGAGAACACATTTACTCCCCAATAATTGTACGGGAGGTGAT CGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCTTTG GCCTTCTCTGAGGTCAGATCGGAACAACTCACTTGAAAAAAAGTCAGGTGGGGGAATGCC AAAAACACAAGCCTTTTGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAG AAAAACACAAGCATTTTGAGAAGAATGGAGAGTCCCTTCATCTCAGGCGGTGGAG Gaps 1, Length 758; 1; Indels 44.8%; Score 730; DB 14; ilarity 99.7%; Pred. No. 1.8e-183; Conservative 0; Mismatches 1; socation/Qualifiers al Similarity 741; Conserv 888 758 948 669 639 1068 579 1128 519 1188 1248 Best Local (Matches 74: Query Match 1008 source FEATURES ORIGIN g ò d à дg 8 8 장 쉼 B & ò g ò

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/tissue_type="Macrophage"
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NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of lowa.
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_ESQ=GGCCATGCG"
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UI-H-FT2-bjk-a-15-0-UI,sl NCI CGAP FT2 Homo sapiens cDNA clone
UI-H-FT2-bjk-a-15-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CHONE Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 746)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
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CF541186 To Dp mRNA linear EST 12-SEP-2003 UI-CF-EC1-adz-a-24-0-UI-3', mRNA sequence.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 710)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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                                                                                                      AAAGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAGGAGGAGCCCA
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Length 746;
                                    Indels
 DB 14;
                  Pred. No. 1.8e-178; ); Mismatches 3;
Score 711.2;
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 43.6%;
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Query Match
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Matches 713; Conservative
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/clone lib="NNIH MGC 115"
/clone lib="NNIH MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                   TGGAGCCTGGCAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAA 1476
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603032387F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173820 5',
                                              350 cagcedregadarcrerererererererereseceaereraceaerere 291
                                                                                                                                                                                                                             Email: cgapbs-ramail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11432 row: m column: 21
High quality sequence start: 8
High quality sequence stop: 739.
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1 (bases 1 to 800)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                        1357 CCGCTCTCCCAGCTGTCTCTCTCTTTTTTTTGGTCAATACACTGAAGATGGAGAATT
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/db_xref="taxon:9606"
/clone="IMAGE:5173820"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-ECI-adz-a-24-0-UI"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="Dife Technologies) (Tl phage resistant)"
/clone lib="UI-CF-ECI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
UI-CF-ECI is a normalized_cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (AT)18 tail. The sequence tag for this library is AAGTGCTTAC.
                        2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cf.html
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0; Mismatches 3; Indels (
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TAG_SEQ=AAGTGCTTAC"
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CA748568 CA748568.1 GI:25568447 EST.
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1 (bases 1 to 687)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                               GAAATCCGCCTCAAAGGGGAAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTT
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                                                        133 TCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTGGGTGAT
                                                                             rcctngggcctgaatgacttgaatgttccccg-ctgagctaacagtccatgtgggggagt
                                                                                                                                                                                                                                                                          AATGATGCTCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGT
                                                                                                                                                                                                                                                                                                                                GAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TICCAGAGCACAGAAGIGAAACACGIGACCAAGGIAGAAIGGAIAITITICAGGACGGCGC
                                                                                                             TCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATTTCAAGATAGAC
                             Gape
                        7;
  Length 800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCCTCGAACACTGGTGACCCCGGCTAGCCTGAAGGCTCTGGTCTTGGG
                           Indels
 Score 682.2; DB 12;
Pred. No. 1e-170;
0; Mismatches 8;
    41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
                               754; Conservative
                Similarity
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    Query Match
                  Best Local
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AUTHORS
TITLE
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                               Matches
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/lab_nost="DHIUB (Lire recomployies)"
/clone lib="NCI_CGAP_FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I;
NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of lowa.

TAG_IIS=UI-H-FT1
TAG_ENBELHUMAN LUNG Aveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_ENBELHUMAN LUNG AVEOLAR MACROPHAGE
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCAGATCGGAACAACTCACTTGAAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCA 1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATATIGATCGTGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGGT
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Pred. No. 9.1e-166;
0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhs-f-08-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.7%;
al Similarity 99.3%;
666; Conservative (
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Best Local Similarity
Matches 666; Conserv
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        Oy
        1380
        TCTCATTGTTTGGTCAATACACTGAAGATTTGGAGCCTGGCAGAGAGACTGGA
        1439

        267
        TCTCATTGTTTGGTCAATACACTGAAGAATTTGGAGCCTGGCAGAGAGACTGGA
        208

        Oy
        1440
        CAGCTCTGGAAGAACAGGCCTGCTGAGGAGCATGGACTTGGCTTTGGATTGG
        1499

        Oy
        1500
        CAGCTCTGGAGGAACAGGCCTGCTGAGGGAGCATGGACTTGGCTTTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGAATAAAAACCA
        1619

        Oy
        1620
        ACCCCAAATCAA
        1619

        Db
        27
        ACCCAAATCAA
        17
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Search completed: October 2, 2004, 05:02:57 Job time: 6335 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 1, 2004, 20:59:40 ; Search time 40 Seconds (without alignments) 947.487 Million cell updates/sec

1 MFCPLKLILLPVLLDYSLGL.....RNNSLEKKSGGGMPKTQQAF 394 US-09-989-728-422 2067 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

coxsackie- and ade hypothetical prote myelin P0 protein limbic-system-assomyelin protein zer sodium channel bet myelin P0 protein myelin P0 protein myelin P0 protein myelin P0 protein sodium channel bet plasmacytoma-assoc SHP substrate-1 preceptor tyrosine hypothetical protein receptor tyrosine hypothetical adhesi Fc gamma (1993) rec protein-tyrosine k myelin P0 protein 50K glycoprotein bypothetical protein sodium call adhesi B-lymphocyte activ secretory componen Fc gamma (1gG) rec protein-tyrosine k hemicentin precurs vascular endotheli Description SUMMARIES JC7780 T08678 A32999 A61087 JC4776 I38053 I61783 JH0252 A29128 A57638 T22889 T43027 S36903 I58375 A54662 JC5519 A53449 JC5288 JC4954 I54766 QRHUGS A57843 Query Match Length DB 1028 509 1040 11232 285 1363 247 338 1379 183 146.5 147 137 132.5 132.5 132.5 125.5 125.5 125.5 125.5 125.5 125.5 125.5 125.5 125.5 125.5 125.5 125.5 128.5 Score Result No.

RESULT 2 T08678

amalgam protein pr fasciclin II precu

SHP substrate-1 pr	Down syndrome cell	T-cell receptor al	B-cell adhesion pr	BIG-1 protein - ra	perlecan precursor	elastic titin - hu	teratocarcinoma ql	connectin 3B - chi	vascular endotheli	junctional adhesio	prequancy-specific	hypothetical prote	heparan sulfate pr	myeloid cell surfa	Fc damma (19G) rec
JC5289	T08851	A53268	JH0371	158164	A38096	I38346	A29915	PN0568	S51656	S56749	176668	T16525	S18252	A30521	S06946
C)	N	N	0	~	~	~	7	7	7	~	7	~	7	~	7
•							_								
513	1896	271	847	1028	4391	7962	330	1323	1348	299	475	662	3707	364	323
5.6 513	•			•	•	•		• •	•	5.2 299			٠,		
	5.6	5.6	5.5	5.5	5.4	5.4	5.3	5.3	5.3		5.2	5.2	5.2	5.2	5.2

ALIGNMENTS

ecepto

cells

SYBULT 1 Weackie- and adenovirus receptor - bovine Weackie- and adenovirus receptor - bovine Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 # Thoelen, 1.; Keyaerts, E.; Lindberg, M.; Van Ranst Ochem. Biophys. Res. Commun. 288, 805-808, 2001 Title: Characterization of a cDNA encoding the bov Reference number: JC7780 Contents: Liver Accession: JC7780 Molecule type: mRNA Residues: 1-36 < THO> Conserves as the primary adenov Comment: This protein serves as the primary adenov B. 9%; Score 183; DB 2; Best Local Similarity 23.9%; Pred. No. 1.1e-0-0; INTRACESCOVEKAVOLIVIVEDEDERINGHYMERGETANLES [:: : : : : : : : : : : : :	Db 285 KSRTSTARSYIGSNHSSLGŚMSPSNMEĠYSKTÓ 317
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Cypace: 10.367, 143-151, 1990

RyBarbu, M.
J. Neurosci. Res. 25, 143-151, 1990

A;Title: Molecular cloning of cDNAs that encode the chicken Po protein: evidence for ear A;Title: Molecular cloning of cDNAs that encode the chicken Po protein: evidence for ear A;Reference number: A61087; MUID: 90204597; PMID: 1690817

A;Reference number: A61087

A;Reference number: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subcontic
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A;Gene: lamp
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termir
C;Keywords: brain; glycoprotein; membrane protein; phosphoprotein
C;Keywords: brain; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 19-May-2000
C;Accession: JC4776
R;Pimenta, A.F.; Fischer, I.; Levitt, P.
Gene 170, 189-195, 1996
A;Title: cDNA cloning and structural analysis of the human limbic-system-associated rA;Title: cDNA cloning and structural analysis of the human limbic-system-associated A;Title: cDNA cloning and structural analysis of the human limbic-system-associated A;Teference number: JC4776; MUID:96235133; PMID:8666243
A;Accession: JC4776
A;Accession: JC4776
A;Residues: 1-338 <PIM>A;Residues: 1-338 <PIM
A;Residues: 1-338 <PIM>A;Residues: 1-338 <PIM
A;Residues: 1-338 <P
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                                                                                                     RVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAA 264
                                                                                                                                                                                                           --K 147
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    --GVPYIEKWGQFRG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myelin P0 glycoprotein precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 VVLHVLPEEPKELMVHVGGLIQMGCVFQSTE-VKHVTKVEWIFSGRRAKEEIVFRYYHKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : : | | : | : : | | : : | | 28 LAIHVY--TPREVYGTVGSHVTLSCSFWSSEWISEDISYTWHFQAEGSRDSISIFHYGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;43-129/Domain: immunoglobulin homology <IMM>
F;154-179/Domain: transmembrane #status predicted <TMM>
F;180-249/Domain: intracellular #status predicted <INT>
F;122/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                            265 LRPLVLGGNQLVIIVGIVCATILLLPVLIL-----IVKKTCGNKSS 305
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                                                                                                                                                                     40 VGSDVTLYCGFWSNEYVSDLTTLSWRFRPDNSRDIISIFHYGN-
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26.8%; Pred. No. 0.0014;
rative 34; Mismatches 70;
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Matches 45; Conservative
                                                                                                                  202
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C;Species: Heterodontus francisci (horn shark)
C;Species: Heterodontus francisci (horn shark)
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: A3299
R;Accession: A3299
R;Accession: A3299
R;Accession: A3299; MulD:90040744; PMID:2478717
A;Reference number: A32999; MulD:90040744; PMID:2478717
A;Reference number: A32999
A;Title: The myelin proteins of the shark brain are similar to the myelin proteins of the A;Reference number: A32999
A;Title: The myelin proteins of the shark brain are similar to the myelin proteins of the A;Reference number: A32999
A;Ccession: A32999
A;Ccession: A32999
A;Molecule type: mRNA
A;Residues: 1-246 <SAA
A;Cross-references: GB:X16714; NID:g63976; PIDN:CAB37865.1; PID:g4467434
C;Superfamily: myelin P0 protein; immunoglobulin homology
C;Keywords: glycoprotein; membrane protein; myelin; Schwann cell; structural protein
F;41-127/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 다
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||::::| : || ||||| : :||::||::||: :||: :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:::||::||::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::|:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGSLLLQDVQEADQGTYIC--EIRL-KGESQVFKKAVVLHVLPEEPKELMVHV--GGLIQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDI 212
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hypothetical protein DKFZp564I1922.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
C;Accession: T08678
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: 216469
A;Accession: T08678
A;Accession: T08678
A;Accession: T08678
A;Accession: T08678
A;Accession: T08678
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A;Accession: T08679
A;Accession: T08679
A;Residues: 1-584 <WAM>
A;Residues: 1-584 <WAM>
A;Residues: 1-584 <WAM>
A;Residues: 1-584 <WAM>
A;Ross-references: EMBL:AL049946
A;Experimental source: fetal brain; clone DKFZp564I1922
C;Genetics:
A;Note: DKFZp564I1922.1
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larity 26.0%; Pred. No. 0.00048;
Conservative 37; Mismatches 61; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 584;
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SLVWVLPNGTDLQSG 343
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Best Local Similarity 21.6%;
Matches 81; Conservative 6
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Best Local S
Matches 44
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Sodium channel beta 2 subunit - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C;Accession: 161783
R;Isom, L.L.; Ragsdale, D.S.; DeJongh, K.S.; Westenbroek, R.E.; Reber, B.F.X.; Scheuer, 7
Cell 83, 433-442, 1995
A;Title: Structure and Function of the Beta 2 Subunit of Brain Sodium Channels, a Transme
A;Reference number: A57843; MUID:96067641; PMID:8521473
A;Accession: 161783
A;Status: preninary; translated from GB/EMBL/DDBJ
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N;Alternate names: myelin protein zero
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence revision 06-Dec-1996 #text_change 16-Jun-2000
C;Accession: JH0252; JN0704; I39378; I58118
R;Hayasaka, K.; Nanao, K.; Tahara, M.; Sato, W.; Takada, G.; Miura, M.; Uyemura, K.
Biochem. Biophys. Res. Commun. 180, 515-518, 1991
A;Title: Isolation and sequence determination of cDNA encoding the major structural prote
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A;Residues: 1-248 <HAY>
A;Residues: 1-248 <HAY>
A;Cross-references: GB:D10537; GB:D90501; NID:g220073; PIDN:BAA01395.1; PID:g220074
A;Experimental source: fetus spinal cord
R;Hayasaka, K.; Ohnishi, A.; Takada, G.; Fukushima, Y.; Murai, Y.
Biochem. Biophys. Res. Commun. 194, 1317-1322, 1993
A;Title: Mutation of the myelin Po gene in charcot-marie-tooth neuropathy type 1.
A;Reference number: JN0704; MUID:93356807; PMID:7688964
                                                                                                            84 K---GOPYIDEVGTFKERIQWVGDPRWKDGSIVIHNLDYSDNGTFTCDVKNPPDIVGKTS 140
                                                                                                                                                                                                        247 -IVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTCGNK-- 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 FONRVHLMGDILCNDGSLLLQDVQEADQGTYICEI----RLKGESQVFKKAVVLHVLPE 138
    QAIVVYT----DREVHGAVGSRVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAISIFHYA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                        KLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 PPELTVHVGDSALMGCVFQS--TEDKCIFKIDWTLSPGEHAKDEYVLYYYSN-LSVPIGR
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                                                                                                                                                                                                                                                                                   ----SSVNSTVLVKNTKKTNPEIKEKPCHFERC 332
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ALQRRLSAMEKGKLHKPGKDASKRGRQTPVLYAQC 223
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A; Molecule type: mRNA
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                                                        188
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                                                      הטיסיבה (Thr) (covalent) #status pred
(Ser) (covalent) #status predicted
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                  F;333-338/Region: hydrophobic
F;40,66,136,148,279,287,300,315/Binding site: carbohydrate (Asn) (covalent) #status
F;42,115,142,164,171,220,231/Binding site: phosphate (Thr) (covalent) #status predic
F;95,192,204,236,310/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence revision 17-May-1996 #text_change 21-Jan-2000
C;Date: 17-May-1996 #sequence revision 17-May-1996 #text_change 21-Jan-2000
C;Accession: I38053; A49643; S43191
R;Rautenstrauss, B.; Nelis, E.; Grehl, H.; Pfeiffer, R.A.; Van Broeckhoven, C.
Hum. Mol. Genet. 3, 1701-1702, 1994
A;Title: Identification of a de novo insertional mutation in P0 in a patient with a A;Reference number: I38053; MUID:95135435; PMID:7530550
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A;Ratus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-251 <RES>
A;Residues: 1-251 <RES>
A;Cross-references: EMBL:Z31718; NID:g469516; PIDN:CAA83513.1; PID:g469517
B;Su, Y.; Brooks, D.G.; Li, L.; Lepercq, J.; Trofatter, J.A.; Ravetch, J.V.; Lebo, Proc. Natl. Acad. Sci. U.S.A. 90, 10856-10860, 1993
A;Title: Myelin protein zero gene mutated in Charcot-Marie-tooth type 1B patients.
A;Reference number: A49643; MUID:94068501; PMID:7504284
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                                                                                                                                                                                                                                                                                                                                                                                                                                               --SLRIQKVDVYDE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTYICEIRLKGESQVFXKAVVLHVLPE---EPKELMVHVGGLIQMGCVFQSTEV----K 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --RAKEEIVFRYYHKLRMSVEY-----SQS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 HLTPTGREFEGEEEYLEILGITREQSGKYECKAANEVSSADVKQVKVTVNYPPTITESKS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----WGHFQNRVNLVG--DIFRNDG--SIMLQGVRESDGG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 NEATTGROASLKCEASAVPAPDFEWYRDDTRINSANGLEIKSTEGOSSLTVTNVTEEHYG 286
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                                                                                                                                                                                                                                                                                                                            13 PLVLLRLCLLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVLEDKNSKVAWLNRSGIIF 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 PLKLILLPVLLDYSLGLN--DLNVSPPELTVHVGDSALMGCVFQSTEDK-----CIF
                                                                                                                                                                                                                      Gaps
                                                                                                                                                           6.6%; Score 137; DB 2; Length 338;
20.1%; Pred. No. 0.0039;
ative 54; Mismatches 123; Indels 110;
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A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
A;Residues: 50-105 <SU1>
A;Experimental source: peripheral blood
A;Note: sequence extracted from NCBI backbone (NCBIP:139777)
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A;Cross-references: GDB:125266; OMIM:159440
A;Map position: 1q22-1q23
C;Superfamily: myelin P0 protein; immunoglobulin homology
F;43-129/Domain: immunoglobulin homology <IMM>
sequence #status predicted <SIG>
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                                                                                                                                                       Query Match 6.6%
Best Local Similarity 20.1%
Matches 72; Conservative
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141 KELMVHVGGLIQMGCVFQSTE-VKHVTKVEWIFSGRRAKEEIVFRYYHKLRMSVEYSQSW 199
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          A, Residuaes 1.246 REAZA
A, Cross-reference number: 13978, MID:94154677; PMID:750928
A, Accession: 13978
A, Accession: 13978
A, Rolled type: DNA
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A29128
myelin PO protein - bovine
C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C; Accession: A29128
R; Sakamoto, Y.; Kitamura, K.; Yoshimura, K.; Nishijima, T.; Uyemura, K.
J; Biol. Chem. 262, 4208-4214, 1987
A; Title: Complete amino acid sequence of PO protein in bovine peripheral nerve myelin.
A; Reference number: A29128; MUID:87166035; PMID:2435734
A; Reference number: A29128
A; Molecule type: protein
A; Residues: 1-219 <SAK>
C; Superfamily: myelin PO protein; immunoglobulin homology
C; Keywords: glycoprotein; membrane protein; myelin; phosphoprotein; Schwann cell; struct
F; 14-100/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 KAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTE-VKHVTKVEWIFSGRRAKEEIVFRYYH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 QAIVVYT----DREVHGAVGSRVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAISFFHYA 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 6.4%; Score 132; DB 1; I Similarity 26.2%; Pred. No. 0.0066; 45; Conservative 31; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 42
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Best Local S
Matches 45
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5.

Gaps

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A;Molecule type: mRNA
A;Residues: 1-248 <LEM2>
C;Comment: This protein is found only in peripheral nervous system Schwann cells.
C;Genetics:
C;Genetics:
A;Introns: 23/1; 78/3; 150/1; 195/2; 215/3
C;Superfamily: myelin P0 protein; immunoglobulin homology
C;Keywords: glycoprotein; myelin; Schwann cell; structural protein; transmembrane protein
C;Keywords: glycoprotein; myelin; Schwann cell; structural protein; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <NAT>
F;30-153/Domain: extracellular #status predicted <EXD>
F;30-153/Domain: immunoglobulin homology <IMM>
F;30-1548/Domain: immunoglobulin homology <IMM>
F;180-248/Domain: intracellular #status predicted <IMD>
F;180-248/Domain: intracellular #status predicted <IMD>
F;122/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: A57843
R;Isom, L.L.; Ragsdale, D.S.; DeJongh, K.S.; Westenbroek, R.E.; Reber, B.F.X.; Scheuer, Cell 83, 433-442, 1995
A;Title: Structure and Function of the Beta 2 Subunit of Brain Sodium Channels, a Transm A;Reference number: A57843; MUID:96067641; PMID:8521473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                major structural protein of perip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myelin PO protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Feb-1995
C;Accession: JQ0622; A22822
R;Lemke, G.; Lamar, E.; Patterson, J.
Neuron 1, 73-83, 1988
A;Title: Isolation and analysis of the gene encoding peripheral myelin protein zero.
A;Reference number: JQ0622; MUID: 90166482; PMID: 2483091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 LRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKT-- 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
29 AIVVYT----DREVYGAVGSQVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAISIFHYAK
                                                                                                                                                                                GHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKT--IVLHVSPEEPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 IVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVK 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 TLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: DNA
A,Residues: 1-248 <LEM>
R;Lemke, G.; Axel, R.
Cell 40, 501-508, 1985
A,Title: Isolation and sequence of a cDNA encoding the n
A;Reference number: A22822; MUID:85124601; PMID:2578885
A;Accession: A22822
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A; Contents: Brain
A; Accession: JC5288
A; Molecule type: mRNA
A; Residues: 1-509 < YAM>
A; Cross-references: DDBJ: D87967; NID: 91864012; PIDN: BAA13520.1; PID: 91864013
C; Comment: This protein is a glycosylated receptor-like protein and plays a role in cell acts as a docking protein and induce translocation of SHP-2 from the cytosol to the plas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-1040 <DEV>
A;Residues: 1-1040 <DEV>
A;Cross-references: GB:U39761; NID:g1079711; PIDN:AAC46934.1; PID:g1079712
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
                        R;Yamao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, Y.; Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A;Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization A;Reference number: JC5287; MUID:97223399; PMID:9070220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 PLRGIANLSNFIRVSPTVKVTQQSPTSMNQVNLTCRAERFYPEDLQLIWLENGNVSRNDT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 SPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCN---DGSLLLQDVQEADQGTYIC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 VKFQKGPSEPDTEIQSGGGTEVYVLAKPSPPEVSGPADRGIPDQKVNFTCKSHGFSPRNI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 PKNL--TKNTDGTYNYTSLFLVNSSAHREDVVFTCQVKHDQ---QPAITRNHTVLGLAHS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GN-----QLVIIVGIVCA--TILLIPVLILIVKKTCGNKSSVNSTVLVK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLRS 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor tyrosine kinase egl-15 precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 24-Sep-1999
C;Accession: A57638
R;DeVore, D.L.; Horvitz, H.R.; Stern, M.J.
Cell 83, 611-620, 1995
A;Title: An FGF receptor signaling pathway is required for the normal cell may Reference number: A57638; MUID:96069862; PMID:7585964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 TLKWFKDGQELHHLETTVNPSGKNVSYNISSTVRV--VLNSMDVHSKVICEVAHITLDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 AKEEIV-FRYYHKLRMSVEYSQSWGHFQNRVNLV---------GDIFRNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMLQGVRESDGG-NYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALR-PLVLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                             4 PLKLILLPVLLDYSLGL--NDLNVSPPELTVHV--GDSALMGCVFQSTEDKCIFKIDWTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDQGSMQTFPGNNATHNWNVFIGVGVACALLVVLLMAALYLLRIKQKKAKGSTSSTRL--
                                                                                                                                                                                                                                                                                                                                                                                                  64; Mismatches 162; Indels 165;
                                                                                                                                                                                                                                                                                                                                                        Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 -------EIRLKGESQV---------
                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                        6.1%; Score 125.5; DE 21.2%; Pred. No. 0.05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453
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A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                       A; Gene: shps-1
A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                             Best Local Sim:
Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
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A;Cross-references: GB:L01991, NID:g200056, PIDN:AAA17403.1, PID:g200057
C;Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              þ
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                                                                                                                                                                                                                                                                                                                                                 84 FONRVHLMGDILCNDGSLLLQDVQEADQGTYICEI----RLKGESQVFKKAVVLHVLPE 138
                                                                                                                                                                                                                                                                                                                                                                             -- LYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTYICEIRLKGESQVFKKAVVLHVLPEEPKELM-----VHVGGLIQMGCVFQSTEVKH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTKVE----WIFSGRRAKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIM 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ALTDFKKDGSHFEK----VGG--SSSGDLM 563
                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                             46
A;Accession: A57843
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Cross-references: EMBL:U37026; NID:g1086496; PIDN:AAC52967.1; PID:g1086497
C;Genetics:
A;Gene: SCNB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHP substrate-1 protein, 509 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 PPELTVHVGDSALMGCVFQS--TEDKCIFKIDWTLSPGEHAKDEYVLYYYSN-LSVPIGR
                                                                                                                                                                                                                                                                                                        PTILSVLNGSDTRLPCTFNSCYTVNHKQFSLNWTYQECSNCSEEMFLQFRMKIINLKLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 SLGLNDLNVSPPELTVHVGDSALMGC------VPQSTEDKCIFKI-DWTLSPGEHAKD
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.1%; Score 126; DB 2; Length 1028; 20.3%; Pred. No. 0.11; ive 49; Mismatches 91; Indels 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change
                                                                                                                                                                             Length
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: A53449
R; Connelly, M.A.; Grady, R.C.; Mushinski, J.F.; Marcu, K.B. Proc. Natl. Acad. Sci. U.S.A. 91, 1337-1341, 1994
A; Title: PANG, a gene encoding a neuronal glycoprotein, is A; Reference number: A53449; MUID: 94151325; PMID: 8108413
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                                                                                                                                                                                                                     65;
                                                                                                                                                                       6.2%; Score 127.5; DB 2; 27.4%; Pred. No. 0.012; iive 28; Mismatches 65;
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Matches 57; Conservative
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Matches 43; Conserv
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hypothetical protein F58A3.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T22889

R;Lennard, N.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19632

A;Accession: T22889

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Generics: CSSP:F58A3.2

A;Generics: C;Generics: A;Generics: CSSP:F58A3.2

A;Introns: 30/1; 50/3; 104/3; 128/1; 245/1; 323/3; 403/3; 457/3; 493/3; 639/2; 665/3; 76

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinasee; protein kinase homolo
                                                                                                                                               23;
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                                                                                                                                                                                                                                                                                                                                                                                                                  VKHVTKVEWIFSGRRAKEEIVFRYYHKLRMSVEYSQSWGHFQN----RVNLVGDIFRNDG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPHII ---WV----RINKINGSYSYYN--NSAEEYMFNYTEMDTFDKAHVHHVGD----ES 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469 TLTIFNVSLDDQGIYACLSGNSLGMSMANATLTVNBFMAIHLLTGDBPKIDRWTTSDYIF 528
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                                                                                                                                                                                                                        |||: ||: || || DYSVSQPVAPDAGLTELNITAEEPP------YFKSNDNIVLFNETHALPAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 PEIKEKPCH--FERCEGEKHIY-----SPIIVREVIEEEEPSEKSEATYMTMH-----P
                                                                                                                                                                                                                                                                                      64 HAK-----DEYVLYYYSN----LSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEA
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                                                                                                                                                                                           15 DYSL------GLNDLNVS---PPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPGE
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                                                                                                                                                 Gaps
                                                                                        Query Match 6.1%; Score 125.5; DB 2; Length 1040; Best Local Similarity 19.9%; Pred. No. 0.12; Matches 85; Conservative 73; Mismatches 150; Indels 119;
                       protein kinase homology <KIN>
protein kinase ATP-binding motif
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C; Keywords: ATP
F; 638-935/Domain:
F; 646-654/Region:
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--VLPEEPKELMVHVGGLIQMGCVFQSTE 161
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Search completed: October 1, 2004, 21:07:31 Job time : 45 secs

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
           Copyright
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- protein search, using sw model OM protein

October 1, 2004, 20:51:10 ; Search time 25 Seconds (without alignments) 820.626 Million cell updates/sec : 0

US-09-989-728-422

Perfect score:

1 MFCPLKLILLPVLLDYSLGL......RNNSLEKKSGGGMPKTQQAF 394 Sequence:

BLOSUM62 Scoring table:

141681 segs, 52070155 residues Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P78310 homo sapien	heter	P97792 mus musculu	gallı	homo s	mus 1	Q13449 homo sapien		aum sum	P25189 homo sapien	pos	P27573 mus musculu	P06907 rattus norv	Q99795 homo sapien	Q9np60 h x-linked	P54900 rattus norv	Q8spv8 pan troglod	Q10656 caenorhabdi	Q63203 rattus norv	Q96pq1 homo sapien	mus mu		pan t	homo	pan t	homo	P12318 homo sapien	P35916 homo sapien	P15364 drosophila	60	O60487 homo sapien	-	E =
SOLINGIA DO	110	CXAR_HUMAN	MYPO_HETFR	CXAR_MOUSE	MYP0_CHICK	CIB2 HUMAN	EVA1 MOUSE	LAMP_HUMAN	LAMP_RAT	IPL2_MOUSE	MYPO_HUMAN	MYP0_BOVIN	MYPO_MOUSE	MYPO_RAT	A33_HUMAN	IPL2_HUMAN	CIB2_RAT	FCGA_PANTR	EG15_CAEEL	FCG2_RAT	SILL_HUMAN	VGR3_MOUSE	LAMP_CHICK	SILL_PANTR		IPL1_PANTR	PIGR_HUMAN	FCGA HUMAN	VGR3_HUMAN	AMAL_DROME	FAS2_SCHAM	EVA1_HUMAN	SHS1_MOUSE	IPL1_MOUSE
5	UB:	-	٦,	-	Н	П	7	Н	Н	Н	H	Н	н	-1	-	-	Н	H	-1	Н	-			-	-	н	Н		-	Н	7	Н	Н	П
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O60469 homo sapien	Q9xt56 bos taurus	Q9nyz4 homo sapien	P59824 rattus norv	P98160 homo sapien	Q90773 gallus gall	P97798 mus musculu	P21995 mus musculu	Q8hxj7 macaca fasc	Ogp2b2 homo sapien	094856 homo sapien	Q9ny72 homo sapien
DSCA HUMAN	JAM1 BOVIN	SIL8 HUMAN	IPL1_RAT	PGBM HUMAN	CEPU_CHICK	NEO1 MOUSE	EMB MOUSE	CIB3 MACFA	FPRP HUMAN	NFAS HUMAN	CIB3_HUMAN
Н	-	Н	Н	Н	Н	Н	Н	-	Н	н	н
2012	298	499	969	4391	353	1493	330	215	879	1240	215
9.6	5.6	5.6	5.6	5.5	5.4	5.4	5.3	5.3	5.3	5.3	5.3
9	5.5	115.5	115	113.5	112	112	110.5	110	109.5	109.5	109
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ALIGNMENTS

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MEDLINE=97250541; PubMed=9096397;
Tomko R.P., Xu R., Philipson L.;
"HCAR and MCAR: the human and mouse cellular receptors for subgroup adenoviruses and group B coxsackieviruses.";
Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Cervix;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Andersson K., Darban H., Oncu D., Mizra M., Sollerbrant K., Sonnhammer E., Philipson L.; "Putative regulatory domains in the human and mouse CAR genes."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=97190109; PubMed=9036860;
Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
"Isolation of a common receptor for Coxsackie B viruses and
                              CXAR HUMAN STANDARD; PRT; 365 AA.
P78310; 000694;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2003 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Coxsackievirus and adenovirus receptor precursor (Coxsackievirus adenovirus receptor) (hCAR) (CVB3 binding protein).
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic organization and chromosomal localization of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.; "Sequence and expression of CXADR, the human gene for the coxsackievirus and adenovirus receptor."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A., Bowles N.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coxsackievirus B-adenovirus receptor gene.";
Hum. Genet. 105:354-359(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=20008750; PubMed=10543405;
                                                                                                                                                                                                                                                                                                                                                        adenoviruses 2 and 5.";
Science 275:1320-1323(1997).
                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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RESULT 1
CXAR_HUMAN
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

Thuman and mouse CDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. P. 99:16993(2002).

-!- SUBGROUP C OF ADENOVIRUSES (ADZ AND ADS).

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SIMILARITY: Contains 2 immunglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 2.
Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR. EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL)
N-LINKED (GLCNAC. . . ) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF200465; AAF24344.1; -. AF242865; AAG01088.1; -. AF242862; AAG01088.1; -. AF242864; AAG01088.1; JOINED. BC003684; AAH03684.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF169361; AAF05908.1; JOINED. AF169362; AAF05908.1; JOINED. AF169363; AAF05908.1; JOINED. AF169364; AAF05908.1; JOINED. AF169365; AAF05908.1; JOINED.
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Genew; HGNC:2559; CXADR.
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162
106
201
365 AA;
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PDB; 1KAC;
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TRANSMEM
DOMAIN
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | | : | || : | || : | || 112 V--KKAPGVANKKIHLVVL-VKPSGARCYVDGSEEIGSDFKIKCEPKEGSLPLQYEW--- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211
                                                                                                                                                                                                                                                            62 GEHAKDEYVLYYYSNLSVPIGRF---QNRVHL-MGDILCNDGSLLLQDVQEADQGTYICE 117
                                                                                                                                                                                                                                                                                                      62 ADNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCK 121
                                                                                                                                                                                                                                                                                                                                                                                                       118 IRLKGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVF----QSTEVKHVTKVEWIFS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 GRRAKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 CSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLI 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTVR--NRVGSDQCLLRLNVVPP------SNKAGLIAGAIIGTLLALALIG 254
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                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 -----ISVKNASSEYSGTYS
                                                                                                                                                                                   LCFVLLCGVVDFA---RSLSITTPERMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISP
                                                                                                          5 LKLILLPVLLDYSLGLNDLNVSPPELTVH--VGDSALMGCVFQ-STEDKCIFKIDWTLSP
                                    Gaps
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01-FEB-1991 (Rel. 17, Last Bequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Myelin PO protein precursor (Myelin protein zero) (Myelin peripheral
protein) (MPP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=900404; PubMed=2478717; Saavedra R.A., Fors L., Aebersold R.H., Arden B., Horvath S., Sanders J., Hood L.; Aebersold R.H., Arden B., Horvath S., Sanders J., Hood L.;

"The myelin proteins of the shark brain are similar to the myelin proteins of the mammalian peripheral nervous system.";
J. Mol. Evol. 29:149-156(1989).
-!- FUNCTION: Creation of an extracellular membrane face which guide the wrapping process and ultimately compacts adjacent lamellae.
-!- SUBCELIULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Found only in peripheral nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes;
Heterodontidae; Heterodontus.
Pred. No. 2e-06;
; Mismatches 148; Indels 100;
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-!- PTM: N-GLYCAN IS SULFATED (BY SIMILARITY).
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Belongs to the myelin P0 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPKSRTSTARSY----IGSNHSSLGSMSPSNMEGYSKTQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 SEKSEATYMTMHPVWPSLRSDRNN--SLEKKSGGGMPKTQ 391
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                                    65;
21.8%;
                                       87; Conservative
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      Similarity
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      Best Local
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                                       Matches
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EMBL; X16714; CAB37865.1; -.

8.1%; Score 168; DB 1; Length 365;

Query Match

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Repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 VGGLIQMGCVFQSTE-VKHVTKVEWIFSGRRAKEEI-VFRYYHKLRMSVEYSQSWGHFQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomko R.P., Xu R., Philipson L.; "HCAR and MCAR: the human and mouse cellular receptors for subgroup adenoviruses and group B coxsackieviruses."; Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
265 LRPLVLGGNQLVIIVGIVCATILLLPVLIL------IVKKTCGNKSS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
N-LINKED (GLCNAC. . .) (COMPLEX)
                                                                                                                                                                                                                                                                                                                                                                                                             Score 146.5; DB 1; Length 246; Pred. No. 7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97190109; PubMed=9036860; Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg "Isolation of a common receptor for Coxsackie B viruses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CXAR MOUSE STANDARD; PRT; 365 AA.
P97792; 009052;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
COXSACKIEVITUS and adenovirus receptor homolog precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                            61; Indels
                                                                                                                                                                                                                                                                                                                                                                            A776A9ED9D430FA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            37; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Liver;
MEDLINE=98080429; PubMed=9420240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                            246 AA; 27335 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           7.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adenoviruses 2 and 5.";
Science 275:1320-1323(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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151
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ID CXAR MC
AC P97792

DT 30-MAY.
DT 30-MAY.
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CS Mus mus CO Mammal:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 GRRAKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYT 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 LIVKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEP 353
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---IREDVP 282
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VV (IN REF. 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GEHAKDEYVLYYSNLSVPIGRF---QNRVHL-MGDILCNDGSLLLQDVQEADQGTYICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 SDNQIVDQVIILYSGDKIYDNYYPDLKGRVHFTSNDVKSGDASINVTNLQLSDIGTYQCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LKLILLPVLLDYSLGLNDLNVSPPELTVH--VGDSALMGCVFQ-STEDKCIFKIDWTLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.1%; Score 146; DB 1; Length 365;
21.8%; Pred. No. 0.00013;
tive 58; Mismatches 155; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [mmunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR
Bergelson J.M., Krithivas A., Celi L., Droguett G., Horwitz M.S., Wickham T., Crowell R.L., Finberg R.W.; "The murine CAR homolog is a receptor for coxsackie B viruses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                 J. Virol. 72:415-419(1998).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5445B4B52A34B2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 SEKSEATYMTMHPVWPSLRSDRNN--SLEKKSGGGMPKTQ 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 GAILFCC------HRKRREEKYEKEVHHD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1201679; Cxadr.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y10320; CAA71368.1; -. EMBL; U90715; AAC53148.1; -. EMBL; Y11929; CAA72679.1; -.
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Best Local Similarity 21.89
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
365
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2338
259
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                                                                                adenoviruses.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 RMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSI-HLGNLVFKKT-I 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GQPYIDDVGSFKERMEWVGNPRRKDGSIVIHNLDYTDNGTFTCDVKNPPDIVGKSSQV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
                                                                        01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Myelin PO protein precursor (Myelin protein zero) (Myelin peripheral protein) (MPP).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 LAIHVY - TPREVYGTVGSHVTLSCSFWSSEWISEDISYTWHFQAEGSRDSISIFHYGK-
                                                                                                                                                                                                                                                                guides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps

evidence for early expression in avians.";
J. Neurosci. Res. 25:143-151(1990).
-!- FUNCTION: Creation of an extracellular membrane face which guide the wrapping process and ultimately compacts adjacent lamellae.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Found only in peripheral nervous system

                                                                                                                                                                                                                                                                                                  C. Schwann cells.
C. -!- SIMILARITY: Belongs to the myelin P0 protein family.
SR PIR; A61087; A61087.
SR PIR; A61087; A61087.
SR InterPro; IPR007110; Ig-like.
SR InterPro; IPR007596; Ig-v.
SR InterPro; IPR00920; Myelin_P0.
SR InterPro; IPR00920; Myelin_P0.
SR InterPro; IPR000920; Myelin_P0.
SR InterPro; IPR000920; Myelin_P0.
SR InterPro; IPR000920; Myelin_P0.
SRART; PR0013; MYELINPO.
DR PROSITE; PS00568; MYELINPO.
DR PROSITE; PS00568; MYELINPO.
SWART; SMO0406; IG-v.
SW Myelin; Structural protein; Glycoprotein; Transmembrane;
KW Phosphorylation; Immunoglobulin domain; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT SIGNAL 30 249 MYELIN P0 PROTEIN.
FT DOMAIN 30 153 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                              "Molecular cloning of cDNAs that encode the chicken PO protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 VLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FBD14801FF8A08FB CRC64;
283 PPKSRTSTARSY----IGSNHSSLGSMSPSNMEGYSKTQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.8%; Score 140.5; DB 1;
26.8%; Pred. No. 0.00022;
. wiematches 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG-LIKE V-TYPE.
                                                      AA.
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CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=90204597; PubMed=1690817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27466 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                      STANDARD;
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143
127
122
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180
30
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50
122
1249 AA;
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Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                       NCBI_TaxID=9031;
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CIB2_HUMAN
ID_CIB2_HUMAN
                                                     CHICK
                                                                                                                                                                                                                    Barbu M.;
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RECUBLINE FROM N.A.

RECUBLINE F. FORDIGH E.A., Grouse L.H., Derge J.G., Schuler G.D., Riausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., R. Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., R.A. Altachul S.F., Jordan H., Woore T., Max S.I., Wang J., Rateh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Schaefer M. J., Oddin T.B., Toshiyuki S., Carninci P., Prange C., Rapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., R. Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., R. Archards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., R. Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., R. Archards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willialon D.K., Muxry D.W., Sodergren E.J., Lu X., Gibbs R.A., Makey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A. Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., R. A. Schein J.E., Jones S.J.M., Marra M.A., Schnetz J., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., R. Schnetch A., Scheni J.E., Jones S.J.M., Marra M.A., Grimwood J., Schmutz J., Marra M.A., Grimmond J.S.A., Ones S.J.M., Marra M.A., Grimmond Sci. U.S.A. 99:16899-16903(2002).

R. PONCTION: Crucial in the assembly, expression, and functional modulation of the heterotrimeric complex of the sodium channel. C. The beta-2 subunit causes an increase in the plasma embrane consulation and in its folding into microvilli (By similarity). C. SUBCNIT: BETA-1 RND BETA-2 SUBUNITS: BETA-1 IS NONCONLENTLY LINKED BY DISULIDE MINE MARCHEN P. R. BETA-1 IS NONCONLENTLY SUBCRILUAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE=99104330; PubMed=9887383;
Bolino A., Seri M., Caroli F., Eubanks J., Srinivasan J., Mandich P.,
Schenone A., Quattrone A., Romeo G., Catterall W.A., Devoto M.;
"Exclusion of the SCN2B gene as candidate for CMT4B.";
Eur. J. Hum. Genet. 6:629-634(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Isom L.L., Mattei L.N., Ragsdale D.S.;
"Primary structure and functional expression of a beta 2 subunit of human infant brain sodium channels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eubanks J., Srinivasan J., Dinulos M.B., Disteche C.M., Catterall W.A.; "Structure and chromosomal localization of the beta2 subunit of the
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cruz J.S., Santana L.F., Frederick C.A., Isom L.L., Malhotra Mattei L.N., Kass R.S., Xia J., An R.-H., Lederer W.J.; "Whether 'slip-mode conductance' occurs."; Science 284:711-711(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                              Sodium channel beta-2 subunit precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97439560; PubMed=9295116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human brain sodium channel.";
NeuroReport 8:2775-2779(1997).
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CHAIN
DOMAIN
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                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 FQDRVEFSGNPSKYDVSVMLRNVQPEDEGIYNCYIMNPPDRHRGHGKIH-----LQVLME 149
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                                                                                                                                                                                                                  EMBL; AF049498; AAC25013.1; -.

EMBL; AF049498; AAC05208.1; -.

EMBL; AF049499; AAC05208.1; -.

EMBL; AF049499; AAC05208.1; -.

EMBL; AF049499; AAC05208.1; -.

EMBL; AF049496; AAC05208.1; -.

EMBL; AF04028; AAP1196.1; -.

EMBL; BC036793; AAP136793.1; -.

EMBL; BC0379; AAP136793.1; -.

EMBL; BC0379; AAP136793.1; -.

EMBL; AAC05203; AAC05203; AAP13679.1

EMBL; BC0379; AAC05203; AAP13679.1

EMBL; AAC0570409; IG; 1.

EMCOPTOLE CHANNELLY COLUMN CHANNEL.

EMPLOSITE: PS550835; IG LIKE; 1.

EMCOPTOLE CHANNEL; SMO0409; IG; 1.

EMCOPTOLE CHANNEL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 PPELITVHVGDSALMGCVFQS--TEDKCIFKIDWTLSPGEHAKDEYVLYYYSN-LSVPIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
SODIUM CHANNEL BETA-2 SUBUNIT.
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE.
POTENTIAL.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
H -> Q (IN REF. 1).
F -> L (IN REF. 1).
T -> S (IN REF. 1).
L -> Q (IN REF. 1).
C -> C (IN REF. 1).
-!- TISSUE SPECIFICITY: Brain specific.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.7%; Score 138.5; DB 1; Length 215; 29.2%; Pred. No. 0.00027; ive 25; Mismatches 60; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94A30A60A32683F3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 41, Created)
(Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24326 MW;
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215 AA;
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les 47; Conserv
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070255;
28-FEB-2003
28-FEB-2003
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DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DISULFID
CARBOHYD
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CONFLICT
SEQUENCE
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SEQUENCE FROM N.A.
STRAIN=RAG-2; TISSUE=Thymus;

XMEDLINE=98252857; PubMed=9585423;

A Guttinger M., Sutti F., Panigada M., Porcellini S., Merati B.,

A Mariani M., Teesalu T., Consalez G.G., Grassi F.;

A Mariani M., Teesalu T., Consalez G.G., Grassi F.;

XI "Epithelial V-like antigen (EVA), a novel member of the immunoglobulin superfamily, expressed in embryonic epithelia with a potential role as homotypic adhesion molecule in thymus histogenesis.";

I Cell Biol. 141:1061-1071(1998).

I Cell Biol. 141:1061-1071(1998).

I Cell Biol. Mediates homophilic cell-cell adhesion.

I SUBCELLULAR LOCATION: Type I membrane protein (Probable).

I TISSUE SPECIFICITY: Expressed in liver and gut, skin, and testis but not in thymocytes, lymphocytes, macrophage or dendritic cells or cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 EIR----LKGESQVFKKAVVLHVLP-EEPKELMVHVGGLIQMGCVFQSTEV--KHVTKVE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
PRINTS; PR00213; MYELINPO.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Cell adhesion; Immunoglobulin domain; Transmembrane; Glycoprotein; Signal.
Signal.
Signal.
1 26 POTENTIAI.
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID±10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG-LIKE V-TYPE.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

F6E5E36787CE69D5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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l Similarity 27.1%; Pred. No. 0.00036;
57; Conservative 33; Mismatches 92; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPITHELIAL V-LIKE ANTIGEN 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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10-OCT-2003 (Rel. 42, Last annotation update)
Epithelial V-like antigen 1 precursor.
EVA1 OR EVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WI-----FSGRRAKEEIVFRYYHKLRMSVE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1289160; Eva.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig v.
InterPro; IPR000920; Myelin_P0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF030454; AAC40128.1; -.
HSSP; P06907; 1NEU.
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39
118
215 AA;
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315
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                      SEQUENCE
                                             Query Match
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LIPID
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                                                                   Matches
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                                                                                                                                                                                         MEDLINE=96235133; PubMed=8666243;

MEDLINE=96235133; PubMed=8666243;

Pimenta A.F., Fischer I., Levitt P.;

"cDNA cloning and structural analysis of the human limbic-system-
associated membrane protein (LAMP).";

Gene 170:189-195(1996).

- !- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.

CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF
MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTH

OF THE HYPPOCAMPAL MOSSY FIBER PROJECTION (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

-!- TISSUE SPECIFICITY: Expressed on limbic neurons and fiber tracts
as well as in single layers of the superior colliculus, spinal
                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                            chord and cerebellum. SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 603241; -. GO: 0007399; P: neurogenesis; TAS.
GO: 0007399; P: neurogenesis; TAS.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 3.
SMART; SM00408; IGc2; 2.
PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor; Repeat; Signal; Lipoprotein.
Repeat; Signal; Lipoprotein.
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                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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LIMBIC SYSTEM-ASSOCIATED MEMBRANE
                                                                                ol-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Limbic system-associated membrane protein precursor (LSAMP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC.
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(GLCNAC.
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(GLCNAC.
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 183 WADRADKAEGTKSKEEEKLNQGNKVSVFVE 212
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N-LINKED ((
N-LINKED (
                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
10-OCT-2003 (Rel. 42, Last ann
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Genew; HGNC:6705; LSAMP.
                                                          STANDARD;
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304
1111
197
290
                                                                                                                                      (Human)
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132
219
219
153
239
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                                                                                                                                      Homo gapiens
                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                     family
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DOMAIN
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                                                HUMAN
                                                         LAMP
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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MEDLINE=95374785; PubMed=7646886;

MEDLINE=95374785; PubMed=7646886;

Pimenta A.F., Zhukareva V., Barbe M.F., Reinoso B.S., Grimley C.,

Henzel W., Fischer I., Levitt P.;

Henzel W., Fischer I., Levitt P.;

The limbic system-associated membrane protein is an Ig superfamily member that mediates selective neuronal growth and axon targeting.";

I member that mediates selective neuronal growth and axon targeting.";

Neuron 15:287-297(1995).

I heuron 15:287-297(1995).

I CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTH OF THE HYPPOCAMPAL MOSSY FIBER PROJECTION.

OF THE HYPPOCAMPAL MOSSY FIBER PROJECTION.

I SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

I SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

I SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

COUNTRIBUTES SELECTION: Attached to the membrane by a GPI-anchor.

I SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

COUNTRIBUTES SELECTION: Attached to the membrane by a GPI-anchor.

COUNTRIBUTES SELECTION: Attached to the membrane by a GPI-anchor.

COUNTRIBUTES SELECTION: Attached to the membrane by a GPI-anchor.

COUNTRIBUTES SELECTION: Attached to the membrane by a GPI-anchor.

COUNTRIBUTES SELECTION: ATTACHED AT E15-16, AT STAGE E20 IT IS DETECTED IN PRESUMPTIVE CORTEX, MEDIAL LIMBIC AREAS OF THE THALAMUS AND HYPOTHALAMUS IN THE ADULT, IT IS FOUND IN THALAMUS AND HYPOTHALAMUS IN THE ADULT, IT IS FOUND IN THALAMUS AND HYPOTHALAMUS IN THE ADULT, IT IS FOUND IN THALAMUS AND HYPOTHALAMUS IN THE ADULT, IT IS FOUND IN THALAMUS AND HYPOTHALAMUS IN THE ADULT, IT IS FOUND IN THALAMUS AND HYPOTHALAMUS IN THE ADULT, IT IS THALAMUS AND HYPOTHALAMUS AND HY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 GSYTCSVQTQHEPKTSQVYLIVQVPPKISNISSDVTVNEGSNVTLVCMANGRPEPVITWR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 HVTKVEWIFSGR-----SQR-----SQR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 HLTPTGREFEGEEEYLEILGITREQSGKYECKAANEVSSADVKOVKVTVNYPPTITESKS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 --KIDWTLSPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTYICEIRLKGESQVFKKAVVLHVLPE---EPKELMVHVGGLIQMGCVFQSTEV----K 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --WGHFQNRVNLVG--DIFRNDG--SIMLQGVRESDGG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 NEATTGRQASLKCEASAVPAPDFEWYRDDTRINSANGLEIKSTEGOSSLTVTNVTEEHYG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 NYTC-----VAANKLGVTNAS----LVLFRPGSVRG-INGSISLAVPLWLLAASLLCL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PLKLILLPVLLDYSLGLN--DLNVSPPELTVHVGDSALMGCVFQSTEDK-----CIF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHALAMUS, PERIRHINAL CORTEX, AMYGDALA AND MEDIAL THALAMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                             54; Mismatches 123; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Limbic system-associated membrane protein precursor (LSAMP)
GPI-anchor amidated asparagine
                                                                                                                                                                                                                   Length 338;
                                                                                                     03455F286DF5D92F CRC64;
                                                                                                                                                                                                              Score 137; DB 1;
Pred. No. 0.00065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 AA
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                                                             (Potential)
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                                                                                                              338 AA; 37308 MW;
                                                                                                                                                                                                                       / Match 6.6%;
Local Similarity 20.1%;
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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        315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                   EMBL; U31554; AAA86120.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 3.
SMART; SM00408; IGc2; 2.
PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor; Repeat; Signal; Lipoprotein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.5%; Score 135; DB 1; Length 338;
19.8%; Pred. No. 0.00095;
ative 55; Mismatches 123; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                  REMOVED IN MATURE FORM (POTENTIAL) IG-LIKE C2-TYPE 1. IG-LIKE C2-TYPE 2. IG-LIKE C2-TYPE 3.
                                                                                                                                                                                                                                                                                                                                                              SYSTEM-ASSOCIATED MEMBRANE
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N-LINKED (GLCNAC. .) (POTENTIAL N-LINKED M-LINKED M-LIN
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 AA; 37324 MW;
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AC Q9ERS6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-LINKED INTERLEUKIN-1 RECEPTOR ACCESSORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oŧ
                                                                                                                                                                                                                                             "Identification and characterization of two members of a novel class of the interleukin-1 receptor (IL-IR) family. Delineation of a new class of IL-IR-related proteins based on signaling.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INCLEASE SERSE-2; Sequence=VSP_008056, VSP_008057;
Note=may be due to an intron retention;
INSUE SPECIFICITY: Detected in fetal brain after day 12.5, in particular in parts of the diencephalon and in the basal plate of the spinal cord. In postnatal brain detected in cerebral cortex, olfactory bulb, in the CA1 region of the hippocampus and in Purkinje cells of the Xth cerebellar lobule.

SIMILARITY: Belongs to the interleukin-1 receptor family.
SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                central
X-linked interleukin-1 receptor accessory protein-like 2 precursor
(ILIRAPL-2 related protein) (TIGIRR-1).
ILIRAPL2.
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO1539; INTRLEUKNIR2.
PRINTS; PRO1537; INTRLEUKNIR1F.
SMART; SM00409; IG; 2.
SMART; SM00255; TIR; 1.
PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS50104; TIR; 1.
Receptor; Repeat; Signal; Transmembrane; Immunoglobulin domain;
                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Brain, and Liver;
MEDLINE=20459050; PubMed=10882729;
Born T.L., Smith D.E., Garka K.E., Renshaw B.R., Bertles J.S.,
                                                                                                                                                                                                                                                                                                                                                                                         Ferrante M.I., Ghiani M., Bulfone A., Franco B., "ILIRAPL2 maps to Xq22 and is specifically expressed in the nervous system.";
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN-LIKE 2.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Type I membrane protein.-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9ERS6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1913106; Illrapl2.
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig.
InterPro; IPR004075; ILl receptor1.
InterPro; IPR004077; ILl receptor1Ip.
InterPro; IPR000157; ILl receptor1Ip.
Pfam; PF00047; ig; 3.
Pfam; PF01582; TIR; 1.
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                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21472256; PubMed=11587848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Slycoprotein; Alternative splicing SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 275:217-221(2001).
                                                                 Mus musculus (Mouse)
                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
355
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                                                                                                                                                                                                                                                                                                                                                                       68 QSTGLRLMWYRNKGDLEEPIIFSEVRMSKEEDAIWFHSAEBQDSGFYTCVLR--NSTYCM 125
                                                                                                                                                                                                                                                                                                                                                                                                           -FSGRR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                   126 KVSMSLTVAENE-----SGLCYNSRIRYLEKSEVTKRKEISCPDMDDFKKSD 172
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01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Myelin PO protein precursor (Myelin protein zero) (Myelin peripheral protein) (MPP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Uyemura K.;
"Isolation and sequence determination of cDNA encoding the major
structural protein of human peripheral myelin.";
                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
DLIYK -> GLLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                           60; Mismatches 130; Indels 114;
                                                                                                                                                                                                                                                  DB 1; Length 686;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                           128 KKAVVLHVLPEEPKELMVHVGGLIQMGCVFQS----TEVKHVTKVEWI
                                                                                                                                                                                                           /FTId=VSP 008057.
36160D1CDE9B8264 CRC64;
 (POTENTIAL)
                                                                                                                                                                                 /FTId=VSP 008056.
Missing (in isoform 2)
            IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
                                                                                                     (GLCNAC.
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Pred. No. 0
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MEDLINE=92062068; PubMed=1719967;
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WEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Pichards S., Worley K.C., Steteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.J., D. Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

H. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.
Koundinya M., Farmer A.;
Phelan M., Farmer A.;
"Cloning of human full-length CDSs in BD Creator(TM) system donor
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MEDLINE=94302675; PubMed=7518101;
Patel P.I., Lupski J.R.;
"Charcot-Marie-Tooth disease: a new paradigm for the mechanism of
                                                                TISSUE=Spinal cord;
MEDLINE=93356807; PubMed=7688964;
Hayasaka K., Ohnishi A., Takada G., Fukushima Y., Murai Y.;
Hayasaka K. ohnishi A. Takada G. Fukushima Y., Murai Y.;
"Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy
                                                                                                                                                                                                                                                   Pham-Dinh D., Fourbil Y., Blanquet F., Mattei M.-G., Roeckel N., Latour P., Chazot G., Vandenberghe A., Dautigny A.; "The major peripheral myelin protein zero gene: structure and localization in the cluster of Fc gamma receptor genes on human
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MEDLINE=95282670; PubMed=7762451;
Roa B.B., Lupski J.R.;
"Molecular genetics of Charcot-Marie-Tooth neuropathy.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                      chromosome 1q21.3-q23.";
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MEDLINE=99103460; PubMed=9888385;
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Van Broeckhoven C.;
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SEQUENCE FROM N.A.
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MEDLINE=94035113; PubMed=7693129; MEDLINE=94035113; PubMed=7693129; MEDLINE=94035113; PubMed=7693129; Mayasaka K., Himoro M., Sato W., Takada G., Uyemura K., Shimizu N., Bird T.D., Conneally P.M., Chance P.F.; Charcot-Marie-Tooth neuropathy type 1B is associated with mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96432254; PubMed=8835320; Blanquet-Grossard F., Pham-Dinh D., Dautigny A., Latour P., Blanquet-Grossard F., Chazot G., Vandenberghe A.; "Charcot-Marie-Tooth type 1B neuropathy: third mutation of serine 63 codon in the major peripheral myelin glycoprotein PO gene.";
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Su Y., Brooks D.G., Li L., Lepercq J., Trofatter J.A., Ravetch J.V.,
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Latour P., Blanquet F., Nelis E., Bonnebouche C., Chapon F.,
Diraison P., Ollagnon E., Dautigny A., Pham-Dinh D., Chazot G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Myelin protein zero gene mutated in Charcot-Marie-Tooth type
                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT CMTIB CYS-82.

MEDLINE=94083941; PubMed=7505151;

Himoro M., Yoshikawa H., Matsui T., Mitsui Y., Takahashi M.,
Kaido M., Nishimura T., Sawaishi Y., Takada G., Hayasaka K.;
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MEDLINE-94100981; PubMed=7506095;
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Hum. Genet. 94:653-657(1994).
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Nat. Genet. 5:31-34(1993)
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MEDLINE=96212920; PubMed=8630052;
Ikegami T., Nicholson G.A., Ikeda H., Ishida A., Johnston H., Wise G.,
Ouvrier R.A., Hayasaka K.;
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glycosylation site in the major peripheral myelin glycoprotein Po.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Myelin P0 protein (Myelin protein zero) (Myelin peripheral protein)
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                              VARIANTS CMT1B THR-135 AND SER-137.
MEDLINE=96263736; PubMed=8664899;
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MEDLINE=87166035; PubMed=2435734;
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                                                                                                                                                        "A novel homozygous mutation of the myelin Po gene producing
Dejerine-Sottas disease (hereditary motor and sensory neuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 6.4%; Score 132; DB 1; Length 248; l Similarity 26.2%; Pred. No. 0.0011; 45; Conservative 31; Mismatches 74; Indels
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Biochem. Biophys. Res. Commun. 222:107-110(1996)
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P10522;
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P06907;
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                                          Date of the control o
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MEDLINE=91244320; PubMed=1709914;
You K.H., Hsieh C.L., Hayes C., Stahl N., Francke U., Popko B.;
"DNA sequence, genomic organization, and chromosomal localization
the mouse peripheral myelin protein zero gene: identification of
polymorphic alleles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
"Complete amino acid sequence of PO protein in bovine peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .) (COMPLEX)
                                                                                                                                                                                        Schwann cells.
-!- PTM: N-GLYCAN IS SULFATED.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Belongs to the myelin P0 protein family.
                                                                                                                                                                                                                                                                                             PIR; A29128; A29128.

HSSP; P06907; INEU.

GlycosuiteDB; P10522; -.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig-v.

InterPro; IPR003596; Ig-v.

InterPro; IPR00313; MYelin P0.

PRINTS; PR00213; MYelin P0.

PROSITE; PS00568; MYELIN P0; 1.

PROSITE; PS00568; MYELIN P0; 1.

Myelin; Structural protein; Glycoprotein; Transmembrane;

Phosphorylation; Immunoglobulin domain.
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PHOSPHORYLATION (BY PKC).
PHOSPHORYLATION (BY PKC).
E4A882C1B7225FAF CRC64;
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01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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Best Local
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MOUSE
MYP0 MC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 SQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTE-VKHVTKVEWIFSGRRAKEEIV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 FRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLV 242
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Genomics 9:751-757(1991).

-I- FUNCTION: Creation of an extracellular membrane face which guides the wrapping process and ultimately compacts adjacent lamellae.

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- TISSUE SPECIFICITY: Found only in peripheral nervous system
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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10-OCT-2003 (Rel. 42, Last annotation update)
Myelin PO protein precursor (Myelin protein zero) (Myelin peripheral
protein) (MPP).
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R HSSP; P06907; INEU.
R MGD; MGI:103177; Mpz.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR000920; Myelin_P0.
R InterPro; IPR000920; Myelin_P0.
R ENINTS; PR00213; MYELINPO.
DR PRINTS; PS00568; MYELINPO.
DR PROSITE; PS00568; MYELIN PO; 1.
DR PROSITE; PS00568; MYELIN PO; 1.
RW Myelin; Structural protein; Glycoprotein; Transmembrane; KW Phosphorylation; Immunoglobulin domain; Signal.
1 29 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I-LINKED (GLCNAC. . .) (COMPLEX) 936D66684300CAC9 CRC64;
                                                                                                                                                                                                                             domain.
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EXTRACELLULAR (BY SIMILARITY)
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CYTOPLASMIC (BY SIMILARITY)
IG-LIKE V-TYPE.
                                                                                                                                                                                   -!- PTM: N-LINKED GLYCAN IS SULFATED.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type do:
-!- SIMILARITY: Belongs to the myelin P0 protein family.
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32; Mismatches
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248 CY
143 IG
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01-JAN-1988 (Rel. 06, Last seq.
10-OCT-2003 (Rel. 42, Last anno
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248 AA;
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Q99795;
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SEQUENCE
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                                                                                                                                                                              Neuron 17:435-449(1996).

-!- FUNCTION: Creation of an extracellular membrane face which guides the wrapping process and ultimately compacts adjacent lamellae.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Found only in peripheral nervous system
                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 30-148.
MEDLINE=96413553; PubMed=8816707;
Shapiro L., Doyle J.P., Hensley P., Colman D.R., Hendrickson W.A.;
"Crystal structure of the extracellular domain from P0, the major structural protein of peripheral nerve myelin.";
                                Lemke G., Axel R.; "Isolation and sequence of a cDNA encoding the major structural protein of peripheral myelin."; Cell 40:501-508(1985).
                                                                                  MEDLINE=90166482; PubMed=2483091;
Lemke G., Lamar E., Patterson J.;
"Isolation and analysis of the gene encoding peripheral myelin
                                                                                                                                                                                                                    Schwann cells.
Schwann cells.
-!- PTM: N-LINKED GLYCAN IS SULFATED.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Belongs to the myelin P0 protein family.
                                                                                                                                                                                                                                                                                                                                               PIRI, JOGG22; MPRTO.
PDB; INEU; 15-MAY-97.
InterPro; IPR00110; Ig-like.
InterPro; IPR003596; Ig-v.
InterPro; IPR00920; Myelin_PO.
PRINTS; PR00213; MYELINPO.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00568; MYELIN PO; 1.
Myelin; Structural protein; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .) (COMPLEX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . G -> R (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE V-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC.
                         MEDLINE=85124601; PubMed=2578885;
                                                                                                                                                                                                                                                                                                                                         EMBL; K03242; AAA41576.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       248
1153
179
248
143
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein zero.";
Neuron 1:73-83(1988).
                                                                    [2]
SEQUENCE FROM N.A.
                SEQUENCE FROM N.A.
NCBI_TaxID=10116;
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30
154
180
30
122
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DOMAIN
TRANSMEM
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CONFLICT
STRAND
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 LRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKT-- 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 ---GOPYIDEVGTFKERIQWVGDPSWKDGSIVIHNLDYSDNGTFTCDVKNPPDIVGKTSQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 AIVVYT----DREVYGAVGSQVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAISIFHYAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen, a novel palmitoylated surface glycoprotein of human gastrointestinal epithelium.";
Biochem. Biophys. Res. Commun. 236:682-686(1997).
-!- FUNCTION: May play a role in cell-cell recognition and signaling.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Expressed in normal gastrointestinal epithelium and in 95% of colon cancers.
-!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED CARBOHYDRATE.
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Colon carcinoma;
MEDLINE=97165045; PubMed=9012807;
Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
Burgess A.W.;
"The human A33 antigen is a transmembrane glycoprotein and a novel
member of the immunoglobulin superfamily.";
Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of posttranslational modifications of human A33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : |: | : | : | : | : | 142 VILYVFEKVPTRY-----GUVULGA-----VIGGILGVVLLLLLLFYLIR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 IVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVK 297
                                                                                                                                                                                                                                                                                                                                                                                                          22;
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Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
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                                                                                                                                                                                                                                                                                                                                Length 248;
                                                                                                                                                                                                                                                                                                                          ch 6.3%; Score 130; DB 1; Length 24 l Similarity 25.1%; Pred. No. 0.0016; 43; Conservative 32; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cell surface A33 antigen precursor (Glycoprotein A33).
                                                                                                                                                                                                                                                        27570 MW; BB703F173466119B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 AA
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Mon Oct

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 LPEEPK---ELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRMS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 PPSKPECGIEGETIIGNNIQLTC--QSKEGSPTPQYSW--------KRYNILNQE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEEPRIL----VIPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTCGNKSSVNST 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 SNEEGTQFCNITVAVRSPSMNVALYVGIAVGVVAALII---IGIIIYCCCCRGKDDNTED 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 LNVSPPE--LTVHVGDSALMGCVPQSTEDKCIFKIDWTLSPGEHAKDEYVLYYYSNLSVP 80
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Q9NPG0; Q9NZNO;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
X-linked interleukin-1 receptor accessory protein-like 2 precursor (ILIRAPL-2 related protein) (Interleukin-1 receptor 9) (IL-1R9) (IL-1 receptor accessory protein-like 2) (Three immunoglobulin domain-containing IL-1 receptor-related 1) (TIGIRR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 VEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKTIVLHVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                             TAS
                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC. .). (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%; Score 128.5; DB 1; Length 319;
                                                                                                   MIM; 602171; -.
GO; GO:0005888; C:proteoglycan integral to plasma membrane;
GO; GO:0004872; F:receptor activity; TAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
                                                                                                                                                                              SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
Transmembrane; Signal; Antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 VLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                  9BFC7AAF45C2408E CRC64;
                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                 SURFACE A33 ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51; Mismatches 141;
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IG-LIKE C2-TYPE.
POLY-CYS.
POTENTIAL.
POTENTIAL.
POTENTIAL.
N-LINKED (GLCNAC.
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                                                                  EMBL; U79725; AAC50957.1;
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Les 73; Conservative
                                                                                  Genew; HGNC:4445; GPA33.
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319 AA;
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236
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257
140
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TRANSMEM
DOMAIN
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MEDLINE=20218565; PubMed=10757639;

Jin H., Viswesvaraiah R., Gardner R.J., Roberts R.G.;

Jin H., Viswesvaraiah R., Gardner R.J., Roberts R.G.;

"Two novel members of the interleukin-1 receptor gene family, one deleted in Xp21.3-Xp21.3 mental retardation.";

Eur. J. Hum. Genet. 8:87-94(2000).

-!- SUBCELLUIAR LOCATION: Type I membrane protein.

-!- SUBCELLUIAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: Detected at low levels in fetal and adult brain, in particular in the frontal lobe, temporal lobe and cerebellum. Detected at very low levels in skin, liver, fetal ovary and in placenta.

-!- SIMILARITY: Belongs to the interleukin-1 receptor family.

-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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                                                                                                                                                                                                                                                                                                                                                                                                              "Identification and characterization of two members of a novel class of the interleukin-1 receptor (IL-1R) family. Delineation of a new class of IL-1R-related proteins based on signaling.";
J. Biol. Chem. 275:29946-29954(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to Xq22.2.";
               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                         TISSUE=Fetal brain;
MEDLINE=20487552; PubMed=11031108;
Sana T.R., Debets R., Timans J.C., Bazan J.F., Kastelein R.A.;
"Computational identification, cloning, and characterization of IL-1R9, a novel interleukin-1 receptor-like gene encoded over an unusually large interval of human chromosome Xq22.2-q22.3.";
Genomics 69:252-262(2000).
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20459050; PubMed=10882729;
Born T.L., Smith D.E., Garka K.E., Renshaw B.R., Bertles J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0004908; F:interleukin-1 receptor activity; TAS. GO; GO:0007417; P:central nervous system development; TAS. InterPro; IPR007110; Ig-like. InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21472256; PubMed=11587848;
Ferrante M.I., Ghiani M., Bulfone A., Franco B.;
"ILIRAPL2 maps to Xq22 and is specifically expressed in nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grabowski M., Lorenz B., Hubel R., Strom T.M.; "A gene (ILIRAPL-2) with 61% identity to ILIRAPL maps to Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                        SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND TISSUE SPECIFICITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 275:217-221(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
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Query Match 6.2%; Score 128; DB 1; Length 686;
Best Local Similarity 20.3%; Pred. No. 0.0091;
Matches 80; Conservative 60; Mismatches 135; Indels 120; Gaps 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 LYY-----YS---NLSVPIGRFQNRVHLMGDILCN------DGSLLLQDVQEADQGTY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 ICEIRLKGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQS----TEVKHVTKVEW 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 I-----FSGRRAKEEIVFRYYHKLRMSVEYSOSWGHFONRVNLVGDIFRNDGSIMLQG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 ISCPDMDDFKKSDQEPDVVWYKECKPRM------WRSI-------IIQKGNALLIQE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 VRESDGGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVII---- 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --VGIVCATILLL----PVL----PVL-311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 VSPPELTVHVGDSALMGCVFQSTEDKCIFK-----IDWTLS-----PGEHAKDEYV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54
                                                                                                                                                                                                            X-LINKED INTERLEUKIN-1 RECEPTOR ACCESSORY PROTEIN-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             524 EAIRACEADULAR (FOIENTIAL).
686 CYTOPLASHIC (POTENTIAL).
686 CYTOPLASHIC (POTENTIAL).
686 IG-LIKE C2-TYPE 1.
632 IG-LIKE C2-TYPE 2.
6347 IG-LIKE C2-TYPE 3.
63 TIR.
63 N-LINKED (GLCNAC. ..) (POTENTIAL).
64 N-LINKED (GLCNAC. ..) (POTENTIAL).
65 N-LINKED (GLCNAC. ..) (POTENTIAL).
66 NM; R400F7ECD186957C CRC64;
                                                                PRINTS; PRO1539; INTRLEUKNIR2.
PRINTS; PRO1539; INTRLEUKNIR1F.
SMART; SM00409; IG; 2.
SMART; SM00255; TIR; 1.
PROSITE; PS50104; TIR; 1.
PROSITE; PS50104; TIR; 1.
Receptor; Repeat; Signal; Transmembrane; Immunoglobulin domain; Glycoprotein.
SIGNAL 1 16 POTENTIAL.
SIGNAL 17 686 X-LINKED INTERLEUKIN-1 RECEPTOR ACC
                                                                                                                                                                                                                              PROTEIN-LIKE 2.
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: October 1, 2004, 21:04:38 Job time: 29 secs
InterPro; IPR004075; IL1_receptor1.
InterPro; IPR004077; IL1_receptorIIp.
InterPro; IPR000157; IIR.
                                          Pfam; PF00047; ig; 3.
Pfam; PF01582; TIR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   686 AA;
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Q86yt9 homo sapien
Q8n37 homo sapien
Q72499 homo sapien
Q8nf70 homo sapien
Q80u19 mus musculu
Q9ygv5 gallus gall
Q9ygv5 gallus gall
Q9ygv1 gallus gall
Q9ygh1 gallus gall
Q9hb4 homo sapien
Q9tu80 canis famil
Q9tu80 canis famil
Q9tu80 rattus norv
Q9tu79 sus scrofa
                                                                                                       October 1, 2004, 20:58:27; Search time 119 Seconds (without alignments) 1044.657 Million cell updates/sec
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                                                                                                                                                                             US-09-989-728-422
2067
1 MFCPLKLILLPVLLDYSLGL.....RNNSLEKKSGGGMPKTQQAF 394
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                               1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: sp_archea:*
2: sp_bacteria:*
3: sp_human:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
7: sp_phage:*
1: sp_phage:*
1: sp_vordent:*
1: sp_vortebrate:*
2: sp_vortebrate:*
3: sp_vortebrate:*
5: sp_vortebrate:*
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Q7Z499
Q8NF70
Q80UL9
Q9YGUS
Q9YGH1
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Q90wi4 gallus gall Q90y50 brachydanio Q8r373 mus musculu Q9uel4 homo sapien O95297 homo sapien P97269 cavia porce Q9r067 rattus norv Q9y3y8 homo sapien Q9lw66 mus musculu Q9uel6 homo sapien Q9ny44 homo sapien Q9ny44 mus musculu Q9iay1 mus musculu Q9iay6 sphorosophila Q8irv9 drosophila Q8irv9 drosophila Q8w4y4 drosophila Q8w4y4 drosophila Q8irv8 drosophila Q8irv8 drosophila Q8irv8 homo sapien Q9w4y4 drosophila Q9w4y4 drosophila Q8w4y4 drosophila Q8w4y4 drosophila Q8irv8 drosophila	0 <u>_</u>
Q90W14 Q90X50 Q8R373 Q9UEL4 O95297 P97269 Q9R066 Q9YR66 Q9UEL6 Q9UEL6 Q9IW14 Q9IA11 Q9IAV6 Q9IRV7 Q8IRV7 Q8IRV9 Q8IRV9 Q8IRV9 Q9IAV4	Q9N2H5 Q8WWT6
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151 150 144 144 150 151 160 160 160 160 160 160 160 160 160 16	
11110222222222222222222222222222222222	4 4

ALIGNMENTS

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Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
Masuho Y., Nagai K., Isogai T.;
"NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RMBL; AK094399; BAC04347.1; -.
RILEFPRO; IPR003599; IG.
RILEFPRO; IPR007110; Ig-like.
RMART; SM00409; IG.
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                              GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT
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IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ37080.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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384 AA; 4
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Matches 378; Conserv
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Q8N917,
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180
                                              305 TKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEBPSEKSEATYMTMHPVWPSLRSD 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDNLCNDGSLLLQDVQEADQGTYLCEIRL 120
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EPRILVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKN 304
                             TKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLRSD 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential.
putative junctional adhesion molecule.
B81F99C929D80C53 CRC64;
                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Bone marrow;
Moog-Lutz C., Cave-Riant F., Guibal F.C., Breau M., Di Gioia Y.,
Cayre Y.E., Lutz P.G.;
"JAML, a novel protein induced in myeloid leukemia cells, has
characteristics of a junctional adhesion molecule.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ515553; CAD56620.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 394;
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                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative junctional adhesion molecule precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sery Match 86.3%; Score 1783; DB 4; set Local Similarity 87.0%; Pred. No. 3.7e-155; tches 354; Conservative 7; Mismatches 20;
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                                                                                                                                                                                             394
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394 AA; 43731 MW;
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 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PGEHAKDEYVLYYYSNLSVPIGRFONRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN 264
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] =
SEQUENCE FROM N.A.
STRAIN=B5/EGFP transgenic ICR mice, TISSUE=Trophoblast Stem Cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
"The nucleotide sequence of a long cDNA clone isolated from human
spleen.";
                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.0%; Score 1364; DB 4; Length 283; Best Local Similarity 99.2%; Pred. No. 7.3e-117; Matches 257; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AK090409; BAC03390.1; -. InterPro; IPR003599; Ig. InterPro; IPR007110; Ig-like. SMART; SM00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 283 AA; 32079 MW; CCACB5B0839EB30E CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                    Last sequence update)
Last annotation update)
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                                                                    Created)
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  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 LVFKKTIVLHVSPEEPRTL 259
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InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
                     Q8NF70;
01-OCT-2002 (TrEMBLrel. 22, Cr
01-OCT-2002 (TrEMBLrel. 22, Lc
01-OCT-2003 (TrEMBLrel. 25, Lc
FLJ00300 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50835; IG_LIKE; 2.
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  PRELIMINARY;
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                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Spleen;
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1D Q8
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DDT 011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LFSKDKDDASEYVLFYYSNLSVPTGRFQNRSHLVGDTFHNDGSLLLQDVQKADEGIYTCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRLKGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIF-SGRR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 AKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 HLGNLVFKKTIVLHVSPEEPRTLVTPAALRPL-----VLGGNQLVIIVGIVCATILLLP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----EKHIYSSITTWET 342
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"CTX, a Xenopus thymocyte receptor, defines a molecular family conserved throughout vertebrates.";
Eur. J. Immunol. 28:4094-4104(1998).
EMBL; AF061023; AAD17523.1; -.
HSSP; P06907; INEU.
InterPro; IPR0031996; Ig.v.
                                                                                                                                                                                                                                                                                                                                   TLSPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICE
                                                                                                                                                                                                                                                                                                      1 MFCPLKLILLPVLL---DYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                               Length 379;
                                                                                                                                                                                        Query Match 47.5%; Score 982; DB 11; Length 37 Best Local Similarity 56.1%; Pred. No. 1.3e-81; Matches 222; Conservative 35; Mismatches 105; Indels
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Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00408; IGc2; 2.
SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE; 2.
SEQUENCE 379 AA; 42561 MW; 2CC0F2987CB12B7F CRC64;
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SEQUENCE 335 AA; 36561 MW; 071A313C3CE6DCA0 CRC64;
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Last annotation update)
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22.1%; Pred. No. 1.2e-09;
tive 74; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 TERGISGE-SEGTYMIMNPVWPS--SPKASSLVRSS 375
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Matches 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  EEEEPSEKSEATYMTMHPVWPSLRSDRNNSLEKKSGGG
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88;
                                                                                                                                                                    171
                                                                                                                                                                                                                                                                                                                                                                                349
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                                                                                                          FYSAKESQLHTIYYYSEQQSYSYGEFKDRI--TAATSPGNASITISNMQPSDTGSYTCEV 117
                                                                                                                                                               RL----KGESQVFKKAVVLHVL--PEEP----KELMVHVGGLIQMGCVFQSTEVKHVTKVE 169
                                                                                                                                                                                          170 WIFSGRRAKEELVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQG-VRESD 228
                                                                                                                                                                                                                                                                                                                                                             289 LPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 CAIVWVLTKKAKKKKSSSNE-MOVMAQKQSNAĖYAQVP-----NEENTPQPAVLPSNA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 LSPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEI 118
                            59
                                                                                                                                                                                                                                                                             MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHV - - GDSALMGCVFQSTEDKCIFKIDWT
                                                                               LSPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEI
                                                                                                                                                                                                                                                                                                                                  229 GGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
Gallus.
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SEQUENCE FROM N.A.
STRAIN=H.B19; TISSUE=Thymus;
Katevuo K.H., Boyd R., Gobel T.T., Bean A., Dunon D., Imhof B.A.,
Vainio O.;
ChTi, a new IgSF member inhibits thymocyte differentiation at the double positive stage.";
Gouble positive stage.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
BMBL; Y14064; CAA74391.1; -.
R HSSP; P06907; INEU.
R INTERPRO; IPR003109; Ig_v.
R InterPro; IPR003596; Ig_v.
R Fam; PF00047; ig; 1.
R SMART; SM00406; IGv; 1.
R SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 13; Length 335; 4.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.3%; Score 192; DB 13; Length 3 22.1%; Pred. No. 4.1e-09; tive 76; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 POTENTIAL.
335 CHT1 THYMOCYTE ANTIGEN.
36509 MW; AA6159598079B438 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : | : | : | : | TNEQPSADEAAASETP-----ENDERHEVQKEETAG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 EEEEPSEKSEATYMTMHPVWPSLRSDRNNSLEKKSGGG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 88; Conserva
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FYSAKESQLHTIYYYSEGQSYSYGEFKDRI--TAATSPGNASITISNMQPSDTGSYTCEV 117
                                                                                       RL----KGESQVFKKAVVLHVL--PEEP---KELMVHVGGLIQMGCVFQSTEVKHVTKVE 169
                                                                                                                                                                                                    170 WIFSGRRAKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQG-VRESD 228
                                                                                                                                                                                                                                                                                                                      229 GGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNOLVIIVGIVCATILL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                       289 LPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 RL----KGESQVFKKAVVLHVL--PEEP---KELMVHVGGLIQMGCVFQSTEVKHVTKVE 169
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                                                                                                                                                                                                                                               |:|| : | : | : | | : | | ESPQDDAGQSQ---KSVIVNVLVKPSKPFCKIEGTPEKGHLIYLLCKCDQ-GLPHPT---
                                                                                                                                                                                                                                                                                                                                                                               205 TGHYRCI--ASNIMGNSTCELDLTSMHSDGNIVAGAL------IGAILAAVII
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=RPRL line 0; TISSUE=Thymus;
Katevuo K.H., Boyd R., Gobel T.T., Bean A., Dunon D., Imhof B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vainio O.;
"ChT1, a new IgSF member inhibits thymocyte differentiation at double positive stage.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y14063; CAA74390.1;
HSSP; P06907; INEU.
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22 335 CHT1 THYMOCYTE ANTIGEN.
335 AA; 36553 MW; AA640C5CD02CB16D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 TNEQPSADEAAA----PETP--ENDEKHEVQKEETAG 332
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Last annotation update)
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354 SEKSEATYMTMHPVWPSLRSDRNN--SLEKKSGGGMPKTQ 391
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                    256 IVFCC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 IRLKGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KE-EIVFRY-YHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCS 235
                                                                                                                                205 TGHYRCI--ASNIMGNSTCELDLTSMHSDGNIVAGAL-------IGAILADVII 249
                                                                                                                                                                                                  289 LPVLILLIVKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVI 348
                                250 CAIVWVLTKKAKKKKSSSNE-MOVMAQKQSNAEYAQVP-----NEENTPATAVLPSNA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
170 WIFSGRRAKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQG-VRESD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                               229 GGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRFLILCGVADFTRG---LSITTPEQMIEKAKGETAYLPCKFTLGPEDQGPLDIEWLLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LKLILLPVLLDYSLGLNDLNVSPPELTVH--VGDSALMGCVFQ-STEDKCIFKIDWTLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21547769; PubMed=11688979;
Thoelen I., Keyaerts E., Lindberg M., Van Ranst M.;
"Characterization of a cDNA encoding the bovine coxsackie and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 8.9%; Score 183; DB 6; Length 365; Local Similarity 23.9%; Pred. No. 3.1e-08; les 95; Conservative 61; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin domain; Receptor.
SEQUENCE 365 AA; 40153 MW; 36DE0BE5DCF88CF9 CRC64;
                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
COXBACKIE virus and adenovirus receptor BCAR.
                                                                                                                                                                                                                                                                                                    349 EEEEPSEKSEATYMTMHPVWPSLRSDRNNSLEKKSGGG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adenovirus receptor...;
Biochem. Biophys. Res. Commun. 288:805-808(2001)
EMBL; AY033651; AAK57804.1; -.
PIR; JC7780; JC7780.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 2. SMART; SM00408; IGC2; 1. PROSITE; PS50835; IG_LIKE; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
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GEHAKDEYVLYYYSNLSVPIGRF---QNRVHL-MGDILCNDGSLLLQDVQEADQGTYICE 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 VKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEFPSE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRRAKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYT 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 LII-FCC-----IREDVP 282
                                                              ---IREDVPPP 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99422053; PubMed=10490761; Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M., Schoemaker H.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P., Lamers J.M.J., Poller W., "Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does not correlate with adenovector targeting in vivo indicating anatomical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LKLILLPVLLDYSLGLNDLNVSPPELTVH--VGDSALMGCVFQ-STEDKCIFKIDWTLSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 168; DB 4; Length 344;
21.8%; Pred. No. 6.9e-07;
Live 65; Mismatches 148; Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 AA; 38097 MW; EEF3722E96C697AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Coxsackie and adenovirus receptor protein (Fragment)
                                                                                                                                                                  285 KSRTSTARSY----IGSNHSSLGSMSDSNMEGYSKTQ 317
                                                                                                                             356 KSEATYMTMHPVWPSLRSDRNN--SLEKKSGGGMPKTQ 391
                                                              ----HKKRREEKYEKEVHHD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene Ther. 6:1520-1535(1999).

EMBL, AF124598; AAD31772.1; -.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR007110; Ig-like.

InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87; Conservative
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us-09-989-728-422.rspt

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SEQUENCE
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Q9H6B4;
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Q9H6B4
                                                 RESULT 12
                                                                                                                   ACCOORDINATE TO THE STANDARD TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||::| |::::::::| GNRITVHGNGSLDIRSLRKS--DSVQLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPIS 2549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WIHVNVOPPKINGNPNPITTVREIAAGGSRKLIDCKAEGIPTPRVLWAFPEGVVLPAPYY 2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 IGRFQNRVHLMGD-----ILCNDGSLLLQDVQEADQGTYIC--EIRL-KGESQVFKK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 AVVLHVLPEEPKELMVHV--GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 VLHVSPEEPRTLVTP---AALRPLVLGGNQLVI---IVGIVCATIL-LLPVLILIVKKTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKTI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNKSSV--NSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEE---EEP-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                                                                                                                                                                                                                Crowl R.M., Luk D.;
"Identification of the gene encoding Adlican, a novel protein expressed in human arthritic tissues.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF245505; AAF86402.1;
HSSP; P56276; ITLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.1%; Score 167; DB 4; Length 2828; 21.8%; Pred. No. 1.5e-05; ive 74; Mismatches 149; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CVFQST--EDKCIFKIDWTLSPG--EHAKD-EYVLYYYSNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2828 AA; 312291 MW; A18377D8554FIFE1 CRC64;
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283 PPKSRISTARSY----IGSNHSSLGSMSPSNMEGYSKTQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKSEATYMTMHPV------WPSLRSDRNNSLEKKSG 384
                                                                                                                                                                       (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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InterPro; IPR003598; Ig c2.
InterPro; IPR001611; IRR.
InterPro; IPR001611; IRR.
InterPro; IPR000483; IRR Cterm.
InterPro; IPR000372; IRR.Nterm.
InterPro; IPR000372; IRR.Typ.
Pfam; PF00047; ig; 12.
Pfam; PF00460; IRR; 6.
Pfam; PF01463; IRRCT; 1.
SMART; SM00408; IGC2; 10.
SMART; SM00082; IRRCT; 1.
SMART; SM0013; IRRT; 1.
SMART; SM0013; IRRT; 1.
SMART; SM00369; IRR TYP; 3.
PROSITE; PS50835; IG LIKE; 12.
Immunoglobulin domain.
SEQUENCE 2828 AA; 312291 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 21.8
les 87; Conservative
                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                           Adlican.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Placenta;
                                                                                                                                                                          01-OCT-2000 (
01-OCT-2000 (
01-OCT-2003 (
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                                                                                                                                                       Q9NR99;
                                                                                     RESULT 11
                                                                                                              Q9NR99
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62 GEHAKDEYVLYYYSNLSVPIGRFON---RVHL-MGDILCNDGSLLLQDVQEADQGTYICE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 ADNQKVDQVILLYSGDKIYDDYYQDLKGRVHFTSNDLKSGDASINVTNLRLSDIGTYQCK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | | | : | | : | | : | | 1.22 V--KKAPGVGNKKIQLTVL-VKPSGIRCYVDGSEEIGNDFKLKCEPKEGSLPLQYEW--- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 LILIVKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 IRLKGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVF----QSTEVKHVTKVEWIFS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 GRRAKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSIHLGNLVFKKTIVLHVSPE--EPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=breed German shepherd; TISSUE=Liver;
MEDLINE=99422053; PubMed=10490761;
Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M., Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P., Lamers J.M.J., Poller W.;
"Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does not correlate with adenovector targeting in vivo indicating anatomical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LKLILLPVLLDYSLGLNDLNVSPPELTVH--VGDSALMGCVFQ-STEDKCIFKIDWTLSP
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                                                                                                                                                                              Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.9%; Score 164; DB 6; Length 319;
Best Local Similarity 22.6%; Pred. No. 1.4e-06;
Matches 91; Conservative 61; Mismatches 146; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 AA; 35422 MW; 85C63A6EC7986965 CRC64;
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                                                   01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-OCT-2003 (TrEMBLrel, 25, Last annotation update)
Coxsackie-adenovirus-receptor homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 EPSEKSEATYMTMHPVWPSLRSDRNN--SLEKKSGGGMPKTQ
  319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BMBL; AF109645; AAF01256.1; ...
GO; GO: GO4872; F: receptor activity; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 2.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 2.
Immunoglobulin domain; Receptor.
NON TER 319 319
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PRELIMINARY;
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                                                                                                                                                                                                                                                                             NCBI_TaxID=9615;
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SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=10090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 LKGE---SQUFKKAVVLHVLPEEPK---ELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GTEPIVY-YWQRIR-----BKEGEDERLPPKSRID----YNHPGRVLLQNLTMSY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
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                                                                                                                                          Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRRAKEEIVFRYYHKLRMSVEYSQSWGHFQ-----NRVNLVGDIFRNDGSIMLQGVRESD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 SGLYQCT--AGNEAGKESCVVRVTVQYVQSI-----GMVAGA-----VTGIVAGALLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 LPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQ-STEDKCIFKIDWTLSPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 GGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.6%; Score 158; DB 4; Length 373;
20.8%; Pred. No. 6.4e-06;
iive 73; Mismatches 132; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                     Eguchi J., Wada J., Hida K., Zhang H.; "Molecular cloning of adipocyte-specific adhesion molecule (ASAM)."; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ22415 (Adipocyte-specific adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 FLLVWLLIRR----ERYE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEERPNEIREDAEAPKARLVKPS--SSSSGSRSSRSGSSSTRS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 EEEEPSE-KSEATYMTMHPVWPSLRSDRNNSLEKKSGGGMPKT 390
                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 NSGRYVWSHVILKVL---VRPSKPKCELEGELTEGSDLTLQCESSS
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Pfam; PF00047; ig; 2.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 2.
Hypothetical protein; Immunoglobulin domain.
SEOUENCE 373 AA; 41280 MW; FDA215EB3B3C4335 CRC64;
                                                                                                                                                                                                                                                                                                                                        EMBL; AKC26068; BAB15347.1; -.
EMBL; BC009371; AAH09371.1; -.
EMBL; AY326422; AAP88386.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      TISSUE=Muscle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Q920S5
ID Q920S5
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Matches
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104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 IVGIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKH 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 IYSPIIVREVIEEEE-----PSEKSEATYMTMHPVWPSLRSDRNNSLEKKSGGGMPK 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 DKCIFKIDWTLSPGEHAKDEYVLY----YYSNLSVPIGRFQNRVHLMGDILCNDGSLLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 DVQEADQGTYICEIRLKGE---SQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 SIMLQGVRESDGGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 -----NEIREDAEAPRARLVKPSSSSGS------RSSRSGSSSTRSTGNSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 TEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRMSVEYSOSWGHF--QNRVNLVGDIFRNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ||| :|: | :: |
237 VTGIVAGALLIFLLIWL-------LIRRKSKDRYEEEDRP-----
                                                                                                                                                                                                                                                                                                                            "Adipocyte-specific protein 5, a novel protein upregulated during adipocyte differentiation."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB040490; BAB68503.1; -.
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11; Length 373;
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OBKIGO;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2003 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Visceral adipose tissue-specific transmembrane protein OL-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.5%; Score 154.5; DB 11; Length 21.2%; Pred. No. 1.3e-05; tive 61; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin domain.
SEQUENCE 373 AA; 41186 MW; 5C6280584AF95326 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adipocyte-specific protein 5.
9030425511RIK OR ASP5.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1918816; 9030425E11Rik.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
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PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 21.2 tes 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 2.
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Q8K1G0
1D Q8K1G0
AC Q8K1G
DT 01-OC
DT 01-OC
DE Visce
OS Rattu
OC Eukar
OC Mamma
OX NCBI
RN [1]
RP SEQUE
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SEQUENCE FROM N.A

A 373

PRT;

PRELIMINARY;

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19;
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C STRAIN=OLETF; TISSUE=Visceral adipose;
Hida K., Wada J., Zhang H., Makino H.;
Hida K., Wada J., Zhang H., Makino H.;
Molecular cloning of visceral adipose tissue-specific gene.";
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EMBL; AF302047; AAM76974.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

R InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.2.

InterPro; IPR003596; Ig.2.

R MART; SM00409; IG; 2.

SMART; SM00409; IG; 2.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 2.

R MANT; SM00406; IGV; 1.

RROSITE; PS50835; IG LIKE; 2.

R MANT; SM00406; IGV; 1.

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R ROSITE; PS50835; IG LIKE; 2.

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